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(57) Abstract

Disclosed are improved broad host range expression vectors wherein gene expression is tightly regulated by tetracycline. The disclosed tetracycline-responsive vectors provide for the creation of stable cell lines, and a method of controlled gene expression where the transient elimination of gene expression is indicated. Also disclosed are tetracycline regulated adenovirus vectors which may be efficiently propagated in 293 cells, along with other tetracycline regulated viral vectors. Also disclosed are methods of using the tetracycline regulated vectors in the treatment of diseases such as cancer.

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DESCRIPTION

VECTORS FOR CONTROLLED GENE EXPRESSION

BACKGROUND OF THE INVENTION

The present application claims the priority of co–pending U.S. Provisional Patent Application Serial No. 60/038,755, filed February 20, 1997, incorporated herein by reference in its entirety without disclaimer.

1. Field of the Invention

The present invention relates generally to the fields of molecular and cellular biology. More particularly, it concerns the field of expression vectors, particularly adenoviral vectors which provide for controlled transcription. Additionally, the present invention concerns the use of the controlled expression adenoviral vectors in situations where regulated expression of a cloned gene of interest is required.

2. Description of Related Art

The key observation that correction of one tumor suppressor gene defect alone in tumors carrying multiple genetic alterations was sufficient to revert their malignant phenotypes sparked off the hopes for cancer gene therapy (Huang *et al.*, 1988; Baker *et al.*, 1990; Klein, 1990). The treatment of human disease by gene transfer has now moved from the theoretical to the practical realm. The first human gene therapy trial was begun in September 1990 and involved transfer of the adenosine deaminase (ADA) gene into lymphocytes of a patient having an otherwise lethal defect in this enzyme, which produces immune deficiency. The results of this initial trial have been very encouraging and have helped to stimulate further clinical trials (Culver *et al.*, 1991).

So far most of the approved gene transfer trials in humans rely on retroviral vectors for gene transduction. Retroviral vectors in this context are retroviruses from which all viral genes have been removed or altered so that no viral proteins are made in cells infected with the vector. Viral replication functions are provided by the use of retrovirus packaging cells that produce all of the viral proteins but that do not produce infectious virus. Introduction of the retroviral vector DNA into packaging cells results in production of virions that carry vector RNA and can infect

target cells, but no further virus spread occurs after infection. To distinguish this process from a natural virus infection where the virus continues to replicate and spread, the term transduction rather than infection is often used. The major advantages of retroviral vectors for gene therapy are the high efficiency of gene transfer into replicating cells, the precise integration of the transferred genes into cellular DNA, and the lack of further spread of the sequences after gene transduction (Miller, 1992).

The potential for production of replication-competent (helper) virus during the production of retroviral vectors remains a concern, although for practical purposes this problem has been solved. So far, most FDA-approved retroviral vectors have been made by using PA317 amphotropic retrovirus packaging cells (Miller *et al.*, 1986). Use of vectors having little or no overlap with viral sequences in the PA317 cells eliminates helper virus production even by stringent assays that allow for amplification of such events (Lynch *et al.*, 1991). Other packaging cell lines are available. For example, cell lines designed for separating different retroviral coding regions onto different plasmids should reduce the possibility of helper virus production by recombination. Vectors produced by such packaging cell lines may also provide an efficient system for human gene therapy (Miller, 1992).

Non-retroviral vectors have also been considered for use in genetic therapy. One such alternative is the adenovirus (Rosenfeld *et al.*, 1992; Jaffe *et al.*, 1992; Lemarchand *et al.*, 1992). Major advantages of adenovirus vectors are their potential to carry large segments of DNA (36 kb genome), a very high titre (10^{11} ml^{-1}), ability to infect non-replicating cells, and suitability for infecting tissues *in situ*, especially in the lung. The most striking use of this vector so far is to deliver a human cystic fibrosis transmembrane conductance regulator (CFTR) gene by intratracheal instillation to airway epithelium in cotton rats (Rosenfeld *et al.*, 1992). However, the adenoviral vectors lack the ability to control gene expression. This can lead to production of toxic gene products before the viral constructs reach the intended destination.

The expression of genes whose products have a harmful effect on the host cell represents a significant problem in the art. Thus the ability to control gene expression is highly desired in a wide variety of expression systems. There are a number of prokaryotic expression vectors that provide controlled gene expression, most notably vectors employing control elements of the *lac*

operon from *E. coli*. In these vectors, gene expression is induced by adding lactose, or a suitable non-cleavable lactose analog, such as isopropyl-β-D-thiogalactopyranoside (IPTG), to the culture medium. While the *lac* system has been shown to function in mammalian cells, the rather slow induction by IPTG results in moderate induction.

A recent system developed to control gene expression relies on tetracycline-responsive promoters (Gossen and Bujard, 1992; U. S. Patent No. 5,464,758). However, while promising, there are a number of problems inherent in this system. Among these are the necessity of using two distinct plasmids to provide the necessary components, and the production of large quantities of the VP16 transcriptional activation region, which can lead to an effect termed "squelching" (Gill and Ptashne, 1988), which can have a deleterious effect on cell growth.

Thus vectors which provide controlled gene expression in a wide variety of systems would represent a significant advance in the art.

SUMMARY OF THE INVENTION

The present invention provides improved broad host range expression vectors wherein gene expression is tightly regulated by tetracycline. The tetracycline-responsive vectors of the present invention provide for the creation of stable cell lines, and a method of controlled gene expression where the transient elimination of gene expression is indicated.

The invention provides a tetracycline responsive expression vector comprising a minimal promoter operatively positioned upstream of a nucleic acid segment comprising a fusion protein gene or a first sequence region encoding a fusion protein comprising a transcriptional transactivation domain operatively attached to a tetracycline repressor protein.

As used herein, the term "minimal promoter" will be understood to include any natural or recombinant promoter or promoter or enhancer fragment, that directs levels of expression of the fusion protein gene encoding a fusion protein comprising a transcriptional transactivation domain operatively attached to a tetracycline repressor protein such that the growth rate of the host cell is not compromised. For example, and not limitation, any promoter which directs expression levels

of about 50% or less compared to the full length CMV promoter in human cells is defined as a "minimal promoter". "Expression levels of about 50% or less" will be understood to encompass expression levels of about 49%, about 48%, about 47%, about 46%, about 45%, about 44%, about 43%, about 42%, about 41%, about 40%, about 39%, about 38%, about 37%, about 36%, about 35%, about 34%, about 33%, about 32%, about 31%, about 30%, about 29%, about 28%, about 27%, about 26%, about 25%, about 24%, about 23%, about 22%, about 21%, about 20%, about 19%, about 18%, about 17%, about 16%, about 15%, about 14%, about 13%, about 12%, about 11%, about 10%, about 9%, about 8%, about 7%, about 6%, about 5%, about 4%, about 3%, about 2%, about 1%, about 0.5%, or about 51%, about 52% or about 53% or so.

The vectors of the instant invention can be regulated by tetracycline or a tetracycline analog. A "tetracycline analog" will be understood to be any one of a number of compounds that are closely related to tetracycline, and which bind to the tet repressor with at least an affinity (K_a) of at least 10^6/M, preferably with a K_a of 10^9/M, and more preferably with a K_a of 10^{11}/M. Exemplary, but in no way limiting, of such tetracycline analogs are those disclosed by Hlavka and Boothe (1985), Mitschef (1978), the Noyee Development Corporation (1969), Evans (1968) and Dowling (1955), each of which is incorporated herein in its entirety.

The invention further provides a tetracycline responsive expression system comprising a first sequence region comprising a fusion protein gene encoding a fusion protein comprising a transcriptional transactivation domain operatively attached to a tetracycline repressor protein, the first sequence region operatively positioned downstream of a minimal promoter; and a second sequence region comprising a cloning site operatively positioned downstream of a basal promoter comprising a tetracycline operator nucleic acid sequence. In one embodiment of the invention the first sequence region and the second sequence region are comprised within a single nucleic acid vector. In another embodiment of the invention the vector further comprises a marker gene encoding a selectable marker protein. In a further embodiment of the invention the marker gene confers resistance to G418.

As used herein, the term "basal promoter" will be understood to include any natural or recombinant promoter or promoter or enhancer fragment, that essentially comprises a "TATA

box", and, in certain embodiments, a transcription start sequence, that alone does not lead to the expression of the nucleic acid segment, sequence region or gene positioned downstream.

In yet another embodiment of the invention the first sequence region is comprised within a first nucleic acid vector, and the second sequence region is comprised within a second distinct nucleic acid vector. In still another embodiment of the invention the first or the second vector further comprises a marker gene encoding a selectable marker protein. In a particular embodiment of the invention the marker gene confers resistance to G418.

In one aspect of the invention the minimal promoter is a minimal CMV promoter/enhancer. In another aspect of the invention the minimal CMV promoter comprises the sequence of SEQ ID NO:7.

An additional embodiment of the invention provides a tetracycline responsive expression system that further comprises a polyadenylation signal functionally positioned downstream of the fusion protein gene. As used herein, the term "gene" is defined as an isolated DNA segment that includes the coding region of a protein, or a portion thereof. Thus the term "gene" includes genomic DNA, cDNA or RNA encoding the protein. In one embodiment of the invention the expression system further comprises a polyadenylation signal functionally positioned downstream of the cloning site.

In another embodiment of the invention the transcriptional activation domain of the fusion protein is a viral transcriptional transactivation domain. In a further embodiment of the invention the transcriptional transactivation domain is from the VP16 protein. In yet another embodiment of the invention the transcriptional activation domain of the fusion protein is a eukaryotic transcriptional transactivation domain. In still another embodiment of the invention the transcriptional transactivation domain is a yeast transcriptional transactivation domain. In a particular embodiment of the invention the transcriptional transactivation domain is from the GAL4, GCN4 or HAP1 protein.

An additional embodiment of the invention provides a tetracycline responsive expression system comprising at least a first exogenous DNA segment inserted into the cloning site. In one

aspect of the invention the first exogenous DNA segment comprises a gene encoding a tumor suppressor protein. In another aspect of the invention the first exogenous DNA segment comprises a gene encoding a retinoblastoma or p53 tumor suppressor protein. In a further aspect of the invention the first exogenous DNA segment comprises a gene encoding a modified retinoblastoma or p53 tumor suppressor protein. As used herein, the term "modified tumor suppressor protein" is defined as a tumor suppressor protein that has at least one amino acid deleted and/or at least one amino acid mutation. The modified tumor suppressor protein may have a biological activity equal to, or even greater than, the biological activity of the corresponding wild-type tumor suppressor protein.

The present invention also provides broad-spectrum modified p53 tumor suppressor proteins that are suprisingly at least as effective, and in most cases more effective, than the corresponding wild-type p53 tumor suppressor proteins in inhibiting cell growth. In particular embodiments, the invention provides p53 tumor suppressor proteins that have a modified N-terminal region. The invention further provides methods of making and using the modified p53 tumor suppressor proteins, particularly in circumstances wherein cell growth inhibition is desired. Thus the present invention provides methods for treating diseases, as exemplified by, but not limited to cancer, that are characterized by abnormal cellular proliferation.

A broad-spectrum tumor suppressor gene is a genetic sequence coding for a protein that, when inserted into and expressed in an abnormally proliferating host cell, *e.g.*, a tumor cell, suppresses abnormal proliferation of that cell irrespective of the cause of the abnormal proliferation.

Thus, the invention provides an isolated DNA segment comprising an isolated gene encoding a modified p53 tumor suppressor protein, the modified p53 tumor suppressor protein comprising an N-terminal modification. The term "N-terminal", or "N-terminal region", as used herein, will be understood to refer to the region of a protein corresponding to as much as the first approximately 40% of the amino acid sequence. Thus, these terms will be understood to include up to about the first 5%, the first 10%, the first 15%, the first 20%, the first 25%, the first 30% or the first 35% of the amino acid sequence of a protein. However, these values are only

approximations, and therefore will be understood to include intermediate values, such as 2%, 3%, 6%, 7%, 11%, 13%, 17%, 18%, 22%, 26%, 33%, 37%, 38%, 41%, 42% and the like.

The term "modified", as used herein, refers to deletions and/or mutations of the wild-type protein sequence. In certain embodiments, it may also refer to insertion of a heterologous amino acid or amino acids into the wild-type protein sequence. In yet other aspects, the term may refer to post-translational alteration of the wild-type amino acid sequence.

In a further embodiment of the invention, the gene encodes a modified p53 tumor suppressor protein comprising an N-terminal region that comprises a first sequence region from which at least one amino acid has been deleted. The deletion may produce a modified p53 tumor suppressor protein with a biological activity equal to, or in certain embodiments, greater than the biological activity of the corresponding wild-type p53 tumor suppressor protein.

In a particular embodiment of the invention the gene encodes a modified p53 tumor suppressor protein wherein at least two amino acids have been deleted from the first sequence region. In other embodiments of the invention at least about five amino acids, at least about ten amino acids, at least about 25 amino acids, at least about 50 amino acids, at least about 75 amino acids or at least about 100 amino acids have been deleted from the first sequence region. It will be understood that intermediate deletion sizes are also contemplated, such as, but not limited to, 3, 4, 6, 7, 8, 9, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98 or 99 amino acids, or even about 101, 102, 103, 104 or 105 amino acids or so.

In one embodiment of the invention the gene encodes a modified p53 tumor suppressor protein comprising an N-terminal region that comprises at least a first sequence region located between about amino acid 1 and about amino acid 50 from which at least one amino acid has been deleted. It will be understood that "between about amino acid 1 and about amino acid 50" includes amino acid 1 and amino acid 50, and it is thus so with other deletions described herein. Amino acid 1 is the N-terminal amino acid, and the numbers increase toward the C-terminus. In

further embodiments of the invention, the first sequence region is located between about amino acid 51 and about amino acid 100, or between about amino acid 1 and about amino acid 100.

Another embodiment of the invention provides a DNA segment comprising an isolated gene encoding a modified p53 tumor suppressor protein comprising an N-terminal modification wherein the gene encodes a modified p53 tumor suppressor protein comprising at least a first N-terminal mutation, and wherein the modified p53 tumor suppressor protein has an increased biological activity in comparison to the biological activity of the corresponding wild type p53 tumor suppressor protein. In a further embodiment of the invention the modified p53 tumor suppressor protein comprises at least a second N-terminal mutation. In a particular embodiment of the invention the gene encodes a modified p53 tumor suppressor protein comprising an N-terminal region from which at least one amino acid has been deleted, and which contains at least one amino acid mutation.

Another embodiment of the invention provides a DNA segment comprising an isolated gene encoding a modified p53 tumor suppressor protein comprising an N-terminal modification, where the DNA segment is operationally positioned under the control of a promoter. In one embodiment of the invention this DNA segment is operationally positioned under the control of a recombinant promoter. In another embodiment of the invention the DNA segment is further defined as a recombinant vector. In a particular aspect of the present invention, the recombinant vector is an adenoviral or retroviral vector. In a further embodiment of the invention the DNA segment is further defined as a component of a tetracycline responsive expression system as described in detail herein. The invention thus provides a modified p53 tumor suppressor protein comprising an N-terminal modification.

In another embodiment of the invention the first exogenous DNA segment comprises a gene encoding a cytokine. In a further embodiment of the invention the gene encodes TNFα. In yet another embodiment of the invention the gene encodes an interferon. In still another embodiment of the invention the gene encodes an interleukin.

An additional embodiment of the invention provides a tetracycline responsive expression system which is comprised within an adenovirus vector. This expression system surprisingly

allows for the propagation of the recombinant adenovirus in 293 cells, which is not though possible with the tetracycline regulated vectors found in the art. In one aspect of the invention the adenovirus vector is comprised within a recombinant adenovirus. In another aspect of the invention the tetracycline responsive expression system is comprised within a retrovirus vector. In a further aspect of the invention the retrovirus vector is comprised within a recombinant retrovirus. In other aspects of the present invention, the tetracycline responsive expression system is comprised within a baculovirus, herpesvirus or adeno-associated virus.

The invention also provides a method for constructing a cDNA library in a tetracycline regulated retrovirus vector, and using the library to screen for novel tumor suppressor genes.

In yet another aspect of the invention the expression system is comprised within a host cell. In one embodiment of the invention the host cell is a prokaryotic host cell. In another embodiment of the invention the host cell is a eukaryotic host cell. In a further embodiment of the invention the host cell is a human cell. In yet another embodiment of the invention the host cell is a tumor cell. In other aspects of the present invention, the host cell is a tumor infiltrating lymphocyte, a bone marrow cell or a hematopoietic stem cell.

An additional embodiment of the invention provides a tetracycline responsive expression system wherein at least a first exogenous DNA segment is inserted into the cloning site, and wherein the first exogenous DNA segment encodes a pharmaceutically active protein. In one embodiment of the invention the first exogenous DNA segment is comprised within a virus vector. In another embodiment of the invention the virus vector is comprised within a virus. In a further embodiment of the invention the virus vector is comprised within a virus and is dispersed in a pharmaceutically acceptable excipient.

The invention thus provides a tetracycline responsive expression system comprising a first nucleic acid vector comprising a minimal promoter operatively positioned upstream of a first sequence region encoding a fusion protein comprising a transcriptional transactivation domain operatively attached to a tetracycline repressor protein; and a second nucleic acid vector comprising a tetracycline operator nucleic acid sequence operatively positioned upstream of a second sequence region comprising a cloning site.

The invention also provides a tetracycline responsive expression vector comprising a first sequence region encoding a fusion protein comprising a transcriptional transactivation domain operatively attached to a tetracycline repressor protein, the first sequence region operatively positioned downstream of a promoter; the vector further comprising a second sequence region comprising a cloning site operatively positioned downstream of a promoter comprising a tetracycline operator nucleic acid sequence.

Additionally, the invention provides a tetracycline responsive expression system comprising a first expression unit comprising a first sequence region encoding a fusion protein comprising a transcriptional transactivation domain operatively attached to a tetracycline repressor protein, the first sequence region operatively positioned downstream of a minimal promoter; the expression system further comprising a second expression unit comprising a second sequence region comprising a cloning site operatively positioned downstream of a promoter comprising a tetracycline operator nucleic acid sequence. The term "expression unit" as used herein is defined as a DNA segment comprising at least a first structural gene, and sufficient promoter and/or enhancer sequences to drive expression of the structural gene or genes. In this regard, "expression unit" and "expression cassette" will be understood to have the same meaning.

The invention provides an improved tetracycline responsive expression system, wherein the improvement comprises the use of a minimal promoter to express a fusion protein comprising a transcriptional transactivation domain operatively attached to a tetracycline repressor protein.

The invention also provides an improved tetracycline responsive expression system comprising a first vector comprising a first expression unit comprising a first sequence region encoding a fusion protein comprising a transcriptional transactivation domain operatively attached to a tetracycline repressor protein, the first sequence region operatively positioned downstream of a promoter, and a second vector comprising a second expression unit comprising a second sequence region comprising a cloning site operatively positioned downstream of a promoter comprising a tetracycline operator nucleic acid sequence, wherein the improvement comprises the use of a minimal promoter having between about 1% and about 50% of the

promoter activity of the CMV promoter when measured in human cells. In one embodiment of the invention the improvement further comprises combining the first expression unit and the second expression unit within a single vector.

"Between about 1% and about 50% of the promoter activity of the CMV promoter" will be understood to include any range within these limits, including between about 1% and about 40%, between about 1% and about 30%, between about 1% and about 25%, between about 1% and about 20%, between about 1% and about 10%, between about 1% and about 5%, between about 5% and about 50%, between about 10% and about 50%, between about 15% and about 50%, between about 20% and about 50%, between about 25% and about 50%, between about 30% and about 50%, between about 40% and about 50%, between about 10% and about 40%, between about 20% and about 30%, between about 5% and about 35%, between about 15% and about 25%, between about 10% and about 20%, between about 40% and about 50%, between about 20% and about 25% or any other intermediate values.

The invention further provides a recombinant host cell comprising a tetracycline responsive expression system comprising a first sequence region comprising an isolated gene encoding a fusion protein comprising a transcriptional transactivation domain operatively attached to a tetracycline repressor protein, the first sequence region operatively positioned downstream of a minimal promoter; and a second sequence region comprising a cloning site operatively positioned downstream of a promoter comprising a tetracycline operator nucleic acid sequence. In one aspect of the invention the cell is a prokaryotic cell. In another aspect of the invention the host cell is a eukaryotic cell. In a further aspect of the invention the host cell is a human cell. In yet another aspect of the invention the human cell is a tumor cell. In other aspects of the present invention, the host cell is a tumor infiltrating lymphocyte, a bone marrow cell or a hematopoietic stem cell.

In one embodiment of the invention the tetracycline responsive expression system is introduced into the cell by means of a recombinant adenovirus vector. In another embodiment of the invention the tetracycline responsive expression system is introduced into the cell by means of a recombinant retrovirus vector.

The invention further provides a pharmaceutical composition comprising a tetracycline responsive expression system comprising a first sequence region encoding a fusion protein comprising a transcriptional transactivation domain operatively attached to a tetracycline repressor protein, the first sequence region operatively positioned downstream of a minimal promoter; and a second sequence region comprising at least a first exogenous DNA segment encoding at least a first pharmaceutically active protein, the exogenous DNA segment operatively positioned downstream of a promoter comprising a tetracycline operator nucleic acid sequence. In one embodiment of the invention the first exogenous DNA segment encodes a wild-type or modified tumor suppressor protein. In another embodiment of the invention the first exogenous DNA segment encodes a cytokine. In a further embodiment of the invention the tetracycline responsive expression system is comprised within a virus vector. In yet another embodiment of the invention the virus vector is comprised within a virus.

The present invention also provides a method of producing a selected protein in a cell, comprising providing to the cell a tetracycline responsive expression system comprising a first sequence region comprising an isolated gene encoding a fusion protein comprising a transcriptional transactivation domain operatively attached to a tetracycline repressor protein, the first sequence region operatively positioned downstream of a minimal promoter; and a second sequence region comprising a nucleic acid segment encoding said selected protein operatively positioned downstream of a promoter comprising a tetracycline operator nucleic acid sequence and collecting the protein produced. In certain aspects, the cell is a prokaryotic cell or a eukaryotic cell. In other embodiments, the selected protein is a tumor suppressor protein or a cytokine. In preferred aspects of the invention, the tetracycline responsive expression system is provided to the cell by means of a recombinant adenovirus vector or a recombinant retrovirus vector.

Thus, the instant tetracycline-responsive vectors and systems of the present invention are contemplated for use in producing a selected protein, for example in a host cell. Therefore, the use of the tetracycline-responsive vectors and systems of present invention for producing a selected protein, for example in a host cell, is provided.

The invention further provides a method of inhibiting cellular proliferation, comprising providing to a cell a tetracycline responsive expression system that expresses an effective amount of a proliferation inhibiting protein in the cell; the expression system comprising a first sequence region comprising an isolated gene encoding a fusion protein comprising a transcriptional transactivation domain operatively attached to a tetracycline repressor protein, the first sequence region operatively positioned downstream of a minimal promoter; and a second sequence region comprising a cloning site for insertion of at least a first exogenous DNA segment, the first exogenous DNA segment encoding the proliferation inhibiting protein, the cloning site operatively positioned downstream of a promoter comprising a tetracycline operator nucleic acid sequence.

In one aspect of the invention the proliferation inhibiting protein is a wild-type or modified tumor suppressor protein. In another aspect of the invention the proliferation inhibiting protein is a cytokine. In a further aspect of the invention the tetracycline responsive expression system is comprised within an adenovirus vector. In yet another aspect of the invention the tetracycline responsive expression system is comprised within a retrovirus vector.

The present invention also provides a method of inhibiting cellular proliferation, comprising providing to a tumor cell a tetracycline responsive expression system that expresses an effective amount of a proliferation inhibiting protein in the cell. In one embodiment of the invention the cell is located within an animal and the cell is provided with the expression system by administering an effective amount of the expression system to the animal in a pharmaceutically acceptable vehicle. In another embodiment of the invention the animal is a human subject. In a further embodiment of the invention the expression system further comprises at least a second exogenous DNA segment that encodes at least a second protein that inhibits cellular proliferation.

The invention also provides a method of treating cancer, comprising administering to an animal with cancer a pharmaceutically acceptable composition comprising a biologically effective inhibitory amount of a first modified p53 tumor suppressor protein that comprises an N-terminal modification.

Thus, the instant tetracycline-responsive vectors and systems of the present invention are contemplated for use in inhibiting cellular proliferation, or in the preparation of a medicament for use in inhibiting cellular proliferation or for treating cancer, for example in a human patient. Therefore, the use of the tetracycline-responsive vectors and systems of present invention for inhibiting cellular proliferation, or in the preparation of a medicament for use in inhibiting cellular proliferation or treating cancer, for example in a human patient, is provided. In certain aspects, the medicaments are formulated for parenteral administration, and in other aspects, the medicaments are intended for administration to a human patient.

The terms "cancer" or "tumor" are clinically descriptive terms which encompass a myriad of diseases characterized by cells that exhibit unchecked and abnormal cellular proliferation. The term "tumor", when applied to tissue, generally refers to any abnormal tissue growth, *i.e.*, excessive and abnormal cellular proliferation. A tumor may be "benign" and unable to spread from its original focus, or "malignant" and capable of spreading beyond its anatomical site to other areas throughout the hostbody. The term "cancer" is an older term which is generally used to describe a malignant tumor or the disease state arising therefrom. Alternatively, the art refers to an abnormal growth as a neoplasm, and to a malignant abnormal growth as a malignant neoplasm.

Irrespective of whether the growth is classified as malignant or benign, the causes of excessive or abnormal cellular proliferation of tumor or cancer cells are not completely clear. Nevertheless, there is persuasive evidence that abnormal cellular proliferation is the result of a failure of one or more of the mechanisms controlling cell growth and division. It is also now believed that the mechanisms controlling cell growth and division include the genetic and tissue-mediated regulation of cell growth, mitosis and differentiation. These mechanisms are thought to act at the cell nucleus, the cell cytoplasm, the cell membrane and the tissue-specific environment of each cell. The process of transformation of a cell from a normal state to a condition of excessive or abnormal cellular proliferation is called tumorigenesis.

It has been observed that tumorigenesis is usually a multistep progression from a normal cellular state to, in some instances, a full malignancy. It is therefore believed that multiple "hits" upon the cell regulatory mechanisms are required for full malignancy to develop. Thus, in most

instances, it is believed that there is no single cause of excessive proliferation, but that these disorders are the end result of a series of cumulative events.

While a malignant tumor or cancer capable of unchecked and rapid spread throughout the body is the most feared and usually the deadliest type of tumor, even so-called benign tumors or growths can cause significant morbidity and mortality by their inappropriate growth. A benign tumor can cause significant damage and disfigurement by inappropriate growth in cosmetically sensitive areas, or by exerting pressure on central or peripheral nervous tissue, blood vessels and other critical anatomical structures.

BRIEF DESCRIPTION OF THE DRAWINGS

The following drawings form part of the present specification and are included to further demonstrate certain aspects of the present invention. The invention may be better understood by reference to one or more of these drawings in combination with the detailed description of specific embodiments presented herein.

FIG. 1. Relative activities of the modified hCMV promoters. The 5637 bladder carcinoma cells (lanes 1-5) and Saos2 osteocarcinoma cells (lanes 6-10) were transfected with reporter plasmids in which CAT gene expression was driven by the various modified (mhCMVp3, lanes 2 and 7; mhCMVp2, lanes 3 and 8; mhCMVp1, lanes 4 and 9) or full-length hCMV promoters (lanes 5 and 10). The % CAT activity is shown on the vertical axis. The CAT activity of the cells transfected with the plasmid carrying the full-length hCMV promoter (lanes 5 and 10) is defined as 100 percent.

FIG. 2. Expression of *tTA* from the modified mCMVp-*tTA* cassette has no squelching effects on the 5637 cell growth. A method of staining cells with crystal violet followed by measuring OD_{550} was used for quantification of relative cell numbers (OD_{550} shown on vertical axis; Gillies *et al.*, 1986). Shown is the growth parent cells with (▲) and without (□) tetracycline, and the mCMVp-*tTA* transfected cells with (♦) and without (○) tetracycline. Days after transfection are shown on the horizontal axis.

FIG. 3A, FIG. 3B and FIG. 3C. The effects of tetracycline-regulatable pRB expression on tumor cell growth (OD_{550}; vertical axis). **FIG. 3A.** Representative long-term clone from the *RB*-reconstituted osteosarcoma cell line (Saos-2, clone 11). **FIG. 3B.** Representative long-term clone from the *RB*-reconstituted breast carcinoma cell line (MDA-MB-468, clone 19-4). **FIG. 3C.** Representative long-term clone from the *RB*-reconstituted bladder carcinoma cell line (5637, clone 34-6). The cells were grown in the presence of 0.5 μg/ml of Tc (□) versus absence of Tc (○). Cell growth of the tumor cells stopped 1 to 2 days after pRB expression was turned on in Tc-free medium (days shown on horizontal axis). The growth cessation was irreversible at day 4 (arrows) after stimulation with fresh medium containing 15% serum (Saos-2), 10% serum plus 2 μg/ml phytohemagglutinin (PHA; MDA-468) or 10% serum plus 4 μg/ml of concanavalin A (Con A; 5637).

FIG. 4A, FIG. 4B and FIG. 4C. The effects of tetracycline-regulatable pRB expression on soft agar colony formation. **FIG. 4A.** Percent colony formation (vertical axis) for three independent Saos2 osteosarcoma cell line clones (RB110 Cl4, lane 2; RB110 Cl11, lane 3; RB110 Cl13, lane 4) and the Saos2 parent strain (lane 1). **FIG. 4B.** Percent colony formation (vertical axis) for two independent MDA-MB-468 breast carcinoma cell line clones (Rb110 Cl19-4, lane 2; Rb110Cl20-1, lane 3) and the MDA-MB-468 parent strain (lane 1). **FIG. 4C.** Percent colony formation (vertical axis) for two independent 5637 bladder carcinoma cell line clones (Rb110 Cl34-6, lane 2; Rb110 Cl36-9, lane 3) and the 5637 parent strain (lane 1). Soft agar colony formation of tumor cells with tetracycline-regulatable pRB expression was completely abrogated by induction of pRB in tetracycline-free medium. Colony formation is shown in the presence (open bar) and the absence (hatched bar) of tetracycline.

FIG. 5. Time course analysis of the pRB^{94} and pRB^{110} expression in representative, Tc-regulatable Saos-2 cell clones in Tc-free media and its effects on DNA synthesis, using a ^{3}H-thymidine incorporation assay. Lack of DNA synthesis as determined by failure of the tumor cells to incorporate thymidine implies growth cessation. The non-synchronized parental Saos-2 cell population (•) maintained steady DNA synthesis; Representative pRB^{110}-reconstituted (▪) and pRB^{94}-reconstituted (♦) Saos-2 clones are illustrated. Percent ^{3}H-labeled cells is shown on the vertical axis, and the hours after removal of tetracycline is shown on the horizontal axis.

FIG. 6. The hTNFα production by the tetracycline-responsive adenovirus vector, AdVtTA.TNFα in transduced human mature T cell line, HUT 78 at different multiplicity of infection (MOI); MOI=200 (•), MOI=100 (♦), MOI=32 (▲), MOI=16 (□) and MOI=200 with 0.1 μg/ml of Tc (○). The hTNFα was quantitated (TNFα concentration in pg/ml shown on the vertical axis) by a standard ELISA assay (Sigma). Time (hours) after infection is shown on the horizontal axis. TNFα secretion from AdVtTA.TNFα-transduced HUT 78 T lymphocytes was vector dose-dependent. Of note, at the highest MOI tested (MOI=200), the leakage expression of TNFα by AdVtTA.TNFα under non-permissive condition (medium containing 0.1 μg/ml tetracycline) was not significant (○).

FIG. 7. The AdVtTA.TNFα-transduced human HUT 78 T cell line secreted high-titer, biologically active human TNFα in the absence of tetracycline. Tetracycline-free conditioned media (▪) collected from the transduced T lymphocytes resulted in potent cytolytic effects on mouse L929 cells (NCTC clone 929, ATCC CCL-1), while conditioned media with 0.1 μg/ml of Tc (•)showed minimal cytolytic effects. Volume of conditioned media (μl) is shown on the horizontal axis, while absorbance (A_{550} - A_{660}) is shown on the vertical axis. Note: L929 is a known TNFα-responsive cell line, and is commonly used for unit definition of biologically active TNFα in the presence of actinomycin D.

FIG. 8. Production of human TNF-α by the Tc-responsive adenovirus vector, AdVtTA.TNFα in transduced human bladder carcinoma cell line 5637. The studies were performed in 24-well plates, ~2.5×10^5 cells were seeded in each well, and different multiplicities of infection (MOI) were tested. MOI=100 (▲), MOI=32 (•), MOI=16(▪) and MOI=100 plus 0.1 μg/ml Tc (♦). Culture media were harvested at different times after AdVtTA.TNFα infection (hours; horizontal axis) and was subjected to a standard TNF-α ELISA analysis (TNF-α production, pg; vertical axis). Most notably, the leakage of TNF-α expression by AdVtTA.TNFα under non-permissive condition (medium containing 0.1 μg/ml of Tc) was not significant, even at the highest MOI tested (MOI=100).

FIG. 9. Transduction of blood progenitor cells by recombinant adenovirus vector AdVtTA.TNFα. Fresh peripheral blood stem cell samples collected from cytapheresis were

maintained in standard culture condition for *ex vivo* expansion of hematopoietic progenitors (Muench *et al.*, 1994), and aliquots of the cell suspension were infected with AdVtTA.TNF-α at different MOI. MOI=100 (▲), MOI=54 (•), MOI=18 (▪) and MOI=100 with 0.1 μg/ml of Tc (♦). TNF-a production (pg) is shown on the vertical axis, and time (hours) after infection is shown on the horizontal axis. The production of TNF-α by the infected cells in Tc-free culture media was vector dose-dependent, and was reduced to near baseline levels in media containing 0.1 μg/ml of Tc. The assays were duplicated and the average amounts of TNF-α detected are shown.

DESCRIPTION OF ILLUSTRATIVE EMBODIMENTS

A. DNA Delivery *via* Infection with Viral Vectors

In certain embodiments of the invention, the tetracycline-regulated expression vectors encoding a selected gene may be stably integrated into the genome of the cell. In yet further embodiments, the vectors may be stably maintained in the cell as a separate, episomal segment of DNA. Such nucleic acid segments or "episomes" encode sequences sufficient to permit maintenance or replication independent of or in synchronization with the host cell cycle. How the expression vector is delivered to a cell and where in the cell the nucleic acid remains is dependent on the type of expression vector employed.

1. Adenoviral Vectors

Preferred for use in the present invention are tetracycline-controlled adenovirus vectors. These vectors may be employed to deliver and express a wide variety of genes, including, but not limited to, tumor suppressor genes such as the retinoblastoma and p53 genes, as well as cytokine genes such as tumor necrosis factor α, the interferon gene family and the interleukin gene family.

A preferred method for delivery of the expression constructs involves the use of an adenovirus expression vector. Although adenovirus vectors are known to have a low capacity for integration into genomic DNA, this feature is counterbalanced by the high efficiency of gene transfer afforded by these vectors. "Adenovirus expression vector" is meant to include those constructs containing adenovirus sequences sufficient to (a) support packaging of the construct in

host cells with complementary packaging functions and (b) to ultimately express a heterologous gene of interest that has been cloned therein.

The expression vector comprises a genetically engineered form of adenovirus. Knowledge of the genetic organization of adenovirus, a 36 kb, linear, double-stranded DNA virus, allows substitution of large pieces of adenoviral DNA with foreign sequences (Grunhaus and Horwitz, 1992). In contrast to retrovirus, the adenoviral infection of host cells does not result in chromosomal integration because wild-type adenoviral DNA can replicate in an episomal manner without potential genotoxicity. Also, adenoviruses are structurally stable, and no genome rearrangement has been detected after extensive amplification.

Adenovirus is particularly suitable for use as a gene transfer vector because of its mid-sized genome, ease of manipulation, high titer, wide target-cell range and high infectivity. Both ends of the viral genome contain 100-200 base pair inverted repeats (ITRs), which are *cis* elements necessary for viral DNA replication and packaging. The early (E) and late (L) regions of the genome contain different transcription units that are divided by the onset of viral DNA replication. The E1 region (E1A and E1B) encodes proteins responsible for the regulation of transcription of the viral genome and a few cellular genes. The expression of the E2 region (E2A and E2B) results in the synthesis of the proteins for viral DNA replication. These proteins are involved in DNA replication, late gene expression and host cell shut-off (Renan, 1990). The products of the late genes, including the majority of the viral capsid proteins, are expressed only after significant processing of a single primary transcript issued by the major late promoter (MLP). The MLP, (located at 16.8 m.u.) is particularly efficient during the late phase of infection, and all the mRNAs issued from this promoter possess a 5'-tripartite leader (TPL) sequence which makes them preferred mRNAs for translation.

In a current system, recombinant adenovirus is generated from homologous recombination between a shuttle vector and a master plasmid which contains the backbone of the adenovirus genome. Due to the possible recombination between the backbone of the adenovirus genome, and the cellular DNA of the helper cells which contain the missing portion of the viral genome, wild-type adenovirus may be generated from this process. Therefore, it is critical to isolate a single clone of virus from an individual plaque and examine its genomic structure.

Generation and propagation of most adenovirus vectors, which are replication deficient, depend on a unique helper cell line, designated 293, which was transformed from human embryonic kidney cells by Ad5 DNA fragments and constitutively expresses E1 proteins (E1A and E1B; Graham *et al.*, 1977). Since the E3 region is dispensable from the adenovirus genome (Jones and Shenk, 1978), the current adenovirus vectors, with the help of 293 cells, carry foreign DNA in either the E1, the E3 or both regions (Graham and Prevec, 1991). In nature, adenovirus can package approximately 105% of the wild-type genome (Ghosh-Choudhury *et al.*, 1987), providing capacity for about 2 extra kb of DNA. Combined with the approximately 5.5 kb of DNA that is replaceable in the E1 and E3 regions, the maximum capacity of most adenovirus vectors is at least 7.5 kb, or about 15% of the total length of the vector. More than 80% of the adenovirus viral genome remains in the vector backbone.

Gene transfer *in vivo* using recombinant E1-deficient adenoviruses results in early and late viral gene expression that may elicit a host immune response, thereby limiting the duration of transgene expression and the use of adenoviruses for gene therapy. In order to circumvent these potential problems, the prokaryotic Cre-loxP recombination system has been adapted to generate recombinant adenoviruses with extended deletions in the viral genome in order to minimize expression of immunogenic and/or cytotoxic viral proteins (Lieber *et al.*, 1996).

Helper cell lines may be derived from human cells such as human embryonic kidney cells, muscle cells, hematopoietic cells or other human embryonic mesenchymal or epithelial cells. Alternatively, the helper cells may be derived from the cells of other mammalian species that are permissive for human adenovirus. Such cells include, *e.g.*, Vero cells or other monkey embryonic mesenchymal or epithelial cells. As stated above, the preferred helper cell line is 293.

Recently, Racher *et al.*, (1995) disclosed improved methods for culturing 293 cells and propagating adenovirus. In one format, natural cell aggregates are grown by inoculating individual cells into 1 liter siliconized spinner flasks (Techne, Cambridge, UK) containing 100-200 ml of medium. Following stirring at 40 rpm, the cell viability is estimated with trypan blue. In another format, Fibra-Cel microcarriers (Bibby Sterlin, Stone, UK) (5 g/l) is employed as follows. A cell inoculum, resuspended in 5 ml of medium, is added to the carrier (50 ml) in a

250 ml Erlenmeyer flask and left stationary, with occasional agitation, for 1 to 4 h. The medium is then replaced with 50 ml of fresh medium and shaking initiated. For virus production, cells are allowed to grow to about 80% confluence, after which time the medium is replaced (to 25% of the final volume) and adenovirus added at an MOI of 0.05. Cultures are left stationary overnight, following which the volume is increased to 100% and shaking commenced for another 72 h.

In some cases, adenovirus mediated gene delivery to multiple cell types has been found to be much less efficient compared to epithelial derived cells. A new adenovirus, AdPK, has been constructed to overcome this inefficiency (Wickham *et al.*, 1996). AdPK contains a heparin-binding domain that targets the virus to heparan-containing cellular receptors, which are broadly expressed in many cell types. Therefore, AdPK delivers genes to multiple cell types at higher efficiencies than unmodified adenovirus, thus improving gene transfer efficiency and expanding the tissues amenable to efficient adenovirus mediated gene therapy.

Other than the requirement that the adenovirus vector be replication defective, or at least conditionally defective, the nature of the adenovirus vector is not believed to be crucial to the successful practice of the invention. The adenovirus may be of any of the 42 different known serotypes or subgroups A-F. Adenovirus type 5 of subgroup C is the preferred starting material in order to obtain the conditional replication-defective adenovirus vector for use in the present invention. This is because Adenovirus type 5 is a human adenovirus about which a great deal of biochemical and genetic information is known, and it has historically been used for most constructions employing adenovirus as a vector.

As stated above, the typical vector according to the present invention is replication defective and will not have an adenovirus E1 region. Thus, it will be most convenient to introduce the foreign gene expression cassette at the position from which the E1-coding sequences have been removed. However, the position of insertion of the construct within the adenovirus sequences is not critical to the invention. The polynucleotide encoding the gene of interest may also be inserted in lieu of the deleted E3 region in E3 replacement vectors as described by Karlsson *et al.*, (1986) or in the E4 region where a helper cell line or helper virus complements the E4 defect (Brough *et al.*, 1996).

Adenovirus growth and manipulation is known to those of skill in the art, and exhibits broad host range *in vitro* and *in vivo*. This group of viruses can be obtained in high titers, *e.g.*, 10^9 to 10^{11} plaque-forming units per ml, and they are highly infective. The life cycle of adenovirus does not require integration into the host cell genome. The foreign genes delivered by adenovirus vectors are episomal and, therefore, have low genotoxicity to host cells. No severe side effects have been reported in studies of vaccination with wild-type adenovirus (Couch *et al.*, 1963; Top *et al.*, 1971), demonstrating their safety and therapeutic potential as *in vivo* gene transfer vectors.

Adenovirus vectors have been used in eukaryotic gene expression (Levrero *et al.*, 1991; Gomez-Foix *et al.*, 1992) and vaccine development (Grunhaus and Horwitz, 1992; Graham and Prevec, 1992). Recently, animal studies suggested that recombinant adenovirus could be used for gene therapy (Stratford-Perricaudet and Perricaudet, 1991; Stratford-Perricaudet *et al.*, 1991; Rich *et al.*, 1993). Studies in administering recombinant adenovirus to different tissues include trachea instillation (Rosenfeld *et al.*, 1991; Rosenfeld *et al.*, 1992), muscle injection (Ragot *et al.*, 1993), peripheral intravenous injections (Herz and Gerard, 1993) and stereotactic inoculation into the brain (Le Gal La Salle *et al.*, 1993). Recombinant adenovirus and adeno-associated virus (see below) can both infect and transduce non-dividing human primary cells.

2. AAV Vectors

Adeno-associated virus (AAV) is also an attractive system for use in construction of tetracycline-regulated vectors for delivery of and expression of selected genes as it has a high frequency of integration and it can infect nondividing cells, thus making it useful for delivery of genes into mammalian cells, for example, in tissue culture (Muzyczka, 1992) or *in vivo*. AAV has a broad host range for infectivity (Tratschin, *et al.*, 1984; Laughlin, *et al.*, 1986; Lebkowski, *et al.*, 1988; McLaughlin, *et al.*, 1988). Details concerning the generation and use of rAAV vectors are described in U.S. Patent No. 5,139,941 and U.S. Patent No. 4,797,368, each incorporated herein by reference.

Studies demonstrating the use of AAV in gene delivery include LaFace *et al.*, (1988); Zhou *et al.*, (1993); Flotte *et al.*, (1993); and Walsh *et al.*, (1994). Recombinant AAV vectors

have been used successfully for *in vitro* and *in vivo* transduction of marker genes (Kaplitt, *et al.*, 1994; Lebkowski, *et al.*, 1988; Samulski, *et al.*, 1989; Yoder, *et al.*, 1994; Zhou, *et al.*, 1994a; Hermonat and Muzyczka, 1984; Tratschin, *et al.*, 1985; McLaughlin, *et al.*, 1988) and genes involved in human diseases (Flotte, *et al.*, 1992; Luo, *et al.*, 1994; Ohi, *et al.*, 1990; Walsh, *et al.*, 1994; Wei, *et al.*, 1994). Recently, an AAV vector has been approved for phase I human trials for the treatment of cystic fibrosis.

AAV is a dependent parvovirus in that it requires coinfection with another virus (either adenovirus or a member of the herpes virus family) to undergo a productive infection in cultured cells (Muzyczka, 1992). In the absence of coinfection with helper virus, the wild type AAV genome integrates through its ends into human chromosome 19 where it resides in a latent state as a provirus (Kotin *et al.*, 1990; Samulski *et al.*, 1991). rAAV, however, is not restricted to chromosome 19 for integration unless the AAV Rep protein is also expressed (Shelling and Smith, 1994). When a cell carrying an AAV provirus is superinfected with a helper virus, the AAV genome is "rescued" from the chromosome or from a recombinant plasmid, and a normal productive infection is established (Samulski, *et al.*, 1989; McLaughlin, *et al.*, 1988; Kotin, *et al.*, 1990; Muzyczka, 1992).

Typically, recombinant AAV (rAAV) virus is made by cotransfecting a plasmid containing the gene of interest flanked by the two AAV terminal repeats (McLaughlin *et al.*, 1988; Samulski *et al.*, 1989; each incorporated herein by reference) and an expression plasmid containing the wild type AAV coding sequences without the terminal repeats, for example pIM45 (McCarty *et al.*, 1991; incorporated herein by reference). The cells are also infected or transfected with adenovirus or plasmids carrying the adenovirus genes required for AAV helper function. rAAV virus stocks made in such fashion are contaminated with adenovirus which must be inactivated by heat shock or physically separated from the rAAV particles (for example, by cesium chloride density centrifugation). Alternatively, adenovirus vectors containing the AAV coding regions or cell lines containing the AAV coding regions and some or all of the adenovirus helper genes could be used (Yang *et al.*, 1994; Clark *et al.*, 1995). Cell lines carrying the rAAV DNA as an integrated provirus can also be used (Flotte *et al.*, 1995).

3. Retr viral Vectors

In particular aspects of the present invention, delivery of selected genes to target cells through the use of retrovirus infection will be desired. Therefore, the inventors contemplate the construction of retroviral expression vectors wherein gene expression is regulated by tetracycline, in a similar manner to that described above.

The retroviruses are a group of single-stranded RNA viruses characterized by an ability to convert their RNA to double-stranded DNA in infected cells by a process of reverse-transcription (Coffin, 1990). The resulting DNA then stably integrates into cellular chromosomes as a provirus and directs synthesis of viral proteins. The integration results in the retention of the viral gene sequences in the recipient cell and its descendants. The retroviral genome contains three genes, gag, pol, and env that code for capsid proteins, polymerase enzyme, and envelope components, respectively. A sequence found upstream from the gag gene contains a signal for packaging of the genome into virions. Two long terminal repeat (LTR) sequences are present at the 5' and 3' ends of the viral genome. These contain strong promoter and enhancer sequences and are also required for integration in the host cell genome (Coffin, 1990).

In order to construct a retroviral vector, a nucleic acid encoding a gene of interest is inserted into the viral genome in the place of certain viral sequences to produce a virus that is replication-defective. In order to produce virions, a packaging cell line containing the gag, pol, and env genes but without the LTR and packaging components is constructed (Mann *et al.*, 1983). When a recombinant plasmid containing a cDNA, together with the retroviral LTR and packaging sequences is introduced into this cell line (by calcium phosphate precipitation for example), the packaging sequence allows the RNA transcript of the recombinant plasmid to be packaged into viral particles, which are then secreted into the culture media (Nicolas and Rubenstein, 1988; Temin, 1986; Mann *et al.*, 1983). The media containing the recombinant retroviruses is then collected, optionally concentrated, and used for gene transfer. Retroviral vectors are able to infect a broad variety of cell types. However, integration and stable expression require the division of host cells (Paskind *et al.*, 1975).

Concern with the use of defective retrovirus vectors is the potential appearance of wild-type replication-competent virus in the packaging cells. This can result from recombination

events in which the intact sequence from the recombinant virus inserts upstream from the gag, pol, env sequence integrated in the host cell genome. However, new packaging cell lines are now available that should greatly decrease the likelihood of recombination (Markowitz *et al.*, 1988; Hersdorffer *et al.*, 1990).

In some cases, the restricted host-cell range and low titer of retroviral vectors can limit their use for stable gene transfer in eukaryotic cells. To overcome these potential difficulties, a murine leukemia virus-derived vector has been developed in which the retroviral envelope glycoprotein has been completely replaced by the G glycoprotein of vesicular stomatitis virus (Burns *et al.*, 1993). These vectors can be concentrated to extremely high titers (10^9 colony forming units/ml), and can infect cells that are ordinarily resistant to infection with vectors containing the retroviral envelope protein. These vectors may facilitate gene therapy model studies and other gene transfer studies that require direct delivery of vectors *in vivo*.

4. Baculoviral Vectors

Baculovirus expression vectors are useful tools for the production of proteins for a variety of applications (Summers and Smith, 1987; O'Reilly *et al.*, 1992; also U.S. Patent Nos., 4,745,051 (Smith and Summers), 4,879,236 (Smith and Summers), 5,077,214 (Guarino and Jarvis), 5,155,037 (Summers), 5,162,222, (Guarino and Jarvis), 5,169,784 (Summers and Oker-Blom) and 5,278,050 (Summers), each incorporated herein by reference). The inventors contemplate the construction of baculoviral expression vectors wherein gene expression is regulated by tetracycline. These vectors might be particularly useful, for example, where the desired protein is toxic to the insect cells. In these instances, production of the protein can be turned off until the cells have reached a very high density, thereby still allowing for the production of large quantities of the desired protein.

Baculovirus expression vectors are recombinant insect vectors in which the coding region of a particular gene of interest is placed behind a promoter in place of a nonessential baculoviral gene. The classic approach used to isolate a recombinant baculovirus expression vector is to construct a plasmid in which the foreign gene of interest is positioned downstream of the *polyhedrin* promoter. Then, *via* homologous recombination, that plasmid can be used to transfer

the new gene into the viral genome in place of the wild-type *polyhedrin* gene (Summers and Smith, 1987; O'Reilly *et al.*, 1992).

The resulting recombinant virus can infect cultured lepidopteran insect cells or larvae and express the foreign gene under the control of the *polyhedrin* promoter, which is strong and provides very high levels of transcription during the very late phase of infection. The strength of the *polyhedrin* promoter is an advantage of the use of recombinant baculoviruses as expression vectors because it usually leads to the synthesis of large amounts of the foreign gene product during infection.

5. Other viral vectors

Other viral vectors may be employed for construction of tetracycline-controlled expression vectors in the present invention. Vectors derived from viruses such as vaccinia virus (Ridgeway, 1988; Baichwal and Sugden, 1986; Coupar *et al.*, 1988), sindbis virus and herpesviruses may be employed. They offer several attractive features for various mammalian cells (Friedmann, 1989; Ridgeway, 1988; Baichwal and Sugden, 1986; Coupar *et al.*, 1988; Horwich *et al.*, 1990).

With the recent recognition of defective hepatitis B viruses, new insight was gained into the structure-function relationship of different viral sequences. *In vitro* studies showed that the virus could retain the ability for helper-dependent packaging and reverse transcription despite the deletion of up to 80% of its genome (Horwich *et al.*, 1990). This suggested that large portions of the genome could be replaced with foreign genetic material. Chang *et al.*, recently introduced the chloramphenicol acetyltransferase (CAT) gene into duck hepatitis B virus genome in the place of the polymerase, surface, and pre-surface coding sequences. It was cotransfected with wild-type virus into an avian hepatoma cell line. Culture media containing high titers of the recombinant virus were used to infect primary duckling hepatocytes. Stable CAT gene expression was detected for at least 24 days after transfection (Chang *et al.*, 1991).

6. Modified Viruses

In still further embodiments of the present invention, particularly wherein delivery of a selected gene to a specific cell type is desired, the tetracycline-responsive expression constructs

to be delivered are housed within an infective virus that has been engineered to express a specific binding ligand. The virus particle will thus bind specifically to the cognate receptors of the target cell and deliver the contents to the cell. A novel approach designed to allow specific targeting of retrovirus vectors was recently developed based on the chemical modification of a retrovirus by the chemical addition of lactose residues to the viral envelope. This modification can permit the specific infection of hepatocytes via sialoglycoprotein receptors.

Another approach to targeting of recombinant retroviruses was designed in which biotinylated antibodies against a retroviral envelope protein and against a specific cell receptor were used. The antibodies were coupled *via* the biotin components by using streptavidin (Roux *et al.*, 1989). Using antibodies against major histocompatibility complex class I and class II antigens, they demonstrated the infection of a variety of human cells that bore those surface antigens with an ecotropic virus *in vitro* (Roux *et al.*, 1989).

B. Other Methods of DNA Delivery

As well as the viral mediated methods of DNA delivery *via* infection of cells described above, other methods of introducing the tetracycline-controlled vectors of the present invention into both prokaryotic and eukaryotic cells are contemplated.

1. Transfection and Transformation

In order to effect expression of a gene construct, the expression construct must be delivered into a cell. As described herein, a preferred mechanism for delivery is *via* viral infection, where the expression construct is encapsidated in an infectious viral particle. However, several non-viral methods for the transfer of expression constructs into eukaryotic and prokaryotic cells also are contemplated by the present invention. In one embodiment of the present invention, the expression construct may consist only of naked recombinant DNA or plasmids. Transfer of the construct may be performed by any of the methods mentioned which physically or chemically permeabilize the cell membrane.

a. Liposome-Mediated Transfection and Transformation

In a further embodiment of the invention, the expression construct may be entrapped in a liposome. Liposomes are vesicular structures characterized by a phospholipid bilayer membrane

and an inner aqueous medium. Multilamellar liposomes have multiple lipid layers separated by aqueous medium. They form spontaneously when phospholipids are suspended in an excess of aqueous solution. The lipid components undergo self-rearrangement before the formation of closed structures and entrap water and dissolved solutes between the lipid bilayers (Ghosh and Bachhawat, 1991). Also contemplated is an expression construct complexed with Lipofectamine (Gibco BRL).

Liposome-mediated nucleic acid delivery and expression of foreign DNA *in vitro* has been very successful (Nicolau and Sene, 1982; Fraley *et al.*, 1979; Nicolau *et al.*, 1987). Wong *et al.*, (1980) demonstrated the feasibility of liposome-mediated delivery and expression of foreign DNA in cultured chick embryo, HeLa and hepatoma cells.

In certain embodiments of the invention, the liposome may be complexed with a hemagglutinating virus (HVJ). This has been shown to facilitate fusion with the cell membrane and promote cell entry of liposome-encapsulated DNA (Kaneda *et al.*, 1989). In other embodiments, the liposome may be complexed or employed in conjunction with nuclear non-histone chromosomal proteins (HMG-1) (Kato *et al.*, 1991). In yet further embodiments, the liposome may be complexed or employed in conjunction with both HVJ and HMG-1.

b. Electroporation

In certain embodiments of the present invention, the expression construct is introduced into the cell *via* electroporation. Electroporation involves the exposure of a suspension of cells and DNA to a high-voltage electric discharge.

Transfection of eukaryotic cells using electroporation has been quite successful. Mouse pre-B lymphocytes have been transfected with human kappa-immunoglobulin genes (Potter *et al.*, 1984), and rat hepatocytes have been transfected with the chloramphenicol acetyltransferase gene (Tur-Kaspa *et al.*, 1986) in this manner.

c. Calcium Phosphate Precipitation or DEAE-Dextran Treatment

In other embodiments of the present invention, the expression construct is introduced to the cells using calcium phosphate precipitation. Human KB cells have been transfected with

adenovirus 5 DNA (Graham and Van Der Eb, 1973) using this technique. Also in this manner, mouse L(A9), mouse C127, CHO, CV-1, BHK, NIH3T3 and HeLa cells were transfected with a neomycin marker gene (Chen and Okayama, 1987), and rat hepatocytes were transfected with a variety of marker genes (Rippe *et al.*, 1990).

In another embodiment, the expression construct is delivered into the cell using DEAE-dextran followed by polyethylene glycol. In this manner, reporter plasmids were introduced into mouse myeloma and erythroleukemia cells (Gopal, 1985).

d. Particle Bombardment

Another embodiment of the invention for transferring a naked DNA expression construct into cells may involve particle bombardment. This method depends on the ability to accelerate DNA-coated microprojectiles to a high velocity allowing them to pierce cell membranes and enter cells without killing them (Klein *et al.*, 1987). Several devices for accelerating small particles have been developed. One such device relies on a high voltage discharge to generate an electrical current, which in turn provides the motive force (Yang *et al.*, 1990). The microprojectiles used have consisted of biologically inert substances such as tungsten or gold beads.

e. Direct Microinjection or Sonication Loading

Further embodiments of the present invention include the introduction of the expression construct by direct microinjection or sonication loading. Direct microinjection has been used to introduce nucleic acid constructs into *Xenopus* oocytes (Harland and Weintraub, 1985), and LTK$^-$ fibroblasts have been transfected with the thymidine kinase gene by sonication loading (Fechheimer *et al.*, 1987).

f. Adenoviral Assisted Transfection

In certain embodiments of the present invention, the expression construct is introduced into the cell using adenovirus assisted transfection. Increased transfection efficiencies have been reported in cell systems using adenovirus coupled systems (Kelleher and Vos, 1994; Cotten *et al.*, 1992; Curiel, 1994).

g. Receptor Mediated Transfection

Still further expression constructs that may be employed to deliver the construct to the target cells are receptor-mediated delivery vehicles. These take advantage of the selective uptake of macromolecules by receptor-mediated endocytosis that will be occurring in the target cells. In view of the cell type-specific distribution of various receptors, this delivery method adds a degree of specificity to the present invention. Specific delivery in the context of another mammalian cell type is described by Wu and Wu (1993; incorporated herein by reference).

Certain receptor-mediated gene targeting vehicles comprise a cell receptor-specific ligand and a DNA-binding agent. Others comprise a cell receptor-specific ligand to which the DNA construct to be delivered has been operatively attached. Several ligands have been used for receptor-mediated gene transfer (Wu and Wu, 1987; Wagner *et al.*, 1990; Perales *et al.*, 1994; Myers, EPO 0273085), which establishes the operability of the technique. In the context of the present invention, the ligand will be chosen to correspond to a receptor specifically expressed on the neuroendocrine target cell population.

In other embodiments, the DNA delivery vehicle component of a cell-specific gene targeting vehicle may comprise a specific binding ligand in combination with a liposome. The nucleic acids to be delivered are housed within the liposome and the specific binding ligand is functionally incorporated into the liposome membrane. The liposome will thus specifically bind to the receptors of the target cell and deliver the contents to the cell. Such systems have been shown to be functional using systems in which, for example, epidermal growth factor (EGF) is used in the receptor-mediated delivery of a nucleic acid to cells that exhibit upregulation of the EGF receptor.

In still further embodiments, the DNA delivery vehicle component of the targeted delivery vehicles may be a liposome itself, which will preferably comprise one or more lipids or glycoproteins that direct cell-specific binding. For example, Nicolau *et al.*, (1987) employed lactosyl-ceramide, a galactose-terminal asialoganglioside, incorporated into liposomes and observed an increase in the uptake of the insulin gene by hepatocytes. It is contemplated that the tissue-specific transforming constructs of the present invention can be specifically delivered into the target cells in a similar manner.

C. Tumor Suppress r and Cytokine Genes

1. Tumor Suppressor Genes

Examples of tumor suppressor genes and candidate tumor suppressor genes contemplated for use in the present invention include, but are not limited to, the retinoblastoma (RB) gene (Friend *et al.*, 1986; Fung *et al.*, 1987; Lee *et al.*, 1987a), the wild-type p53 gene (Finlay *et al.*, 1989; Baker *et al.*, 1990), the deleted in colon carcinoma (DCC) gene (Fearon *et al.*, 1990a; 1990b), the neurofibromatosis type 1 (NF-1) gene (Wallace *et al.*, 1990; Viskochil *et al.*, 1990; Cawthon *et al.*, 1990), the Wilms tumor (WT-1) gene (Call *et al.*, 1990; Gessler *et al.*, 1990; Pritchard-Jones *et al.*, 1990), the von Hippel-Lindau (VHL) disease tumor suppressor gene (Duan *et al.*, 1995), the Maspin (Zou *et al.*, 1994), Brush-1 (Schott *et al.*, 1994) and BRCA 1 genes (Miki *et al.*, 1994; Futreal *et al.*, 1994) for breast cancer, and the multiple tumor suppressor (MTS) or p16 gene (Serrano *et al.*, 1993; Kamb *et al.*, 1994).

a. Retinoblastoma

Based upon study of the isolated RB cDNA clone, the predicted RB gene product has 928 amino acids and an expected molecular weight of 106 kDa (Lee *et al.*, 1987a; 1987b). The natural factor corresponding to the predicted RB gene expression product has been identified as a nuclear phosphoprotein having an apparent relative molecular mass (M_r) of between 105 and 114 kDa (Lee *et al.*, 1987b; Xu *et al.*, 1989b; Yokota *et al.*, 1988; Whyte *et al.*, 1988). The literature generally refers to the protein encoded by the RB gene as $p110^{RB}$. On SDS-PAGE normal human cells show an RB protein pattern consisting of a lower sharp band with an Mr of 110 kD and a broader, more variable region above this band with an M_r ranging from 110 kD to 116 kD. The 110 kD band is the underphosphorylated RB protein, whereas the broader region represents the phosphorylated RB protein. The heterogeneity of the molecular mass results from a varying degree of phosphorylation (Xu *et al.*, 1989b).

After years of intense scrutiny, the biological functions of the RB gene are beginning to be understood (reviewed in Cooper and Whyte, 1989; Hamel *et al.*, 1993; Horowitz, 1993; Riley *et al.*, 1994; Wang *et al.*, 1994; Weinberg, 1995). The RB protein shows cyclical changes in phosphorylation during the cell cycle. Most RB protein is unphosphorylated during G1 phase, but most (perhaps all) RB molecules are phosphorylated in S and G2 phases (Xu *et al.*, 1989b;

DeCaprio *et al.*, 1989; Buchkovich *et al.*, 1989; Chen *et al.*, 1989; Mihara *et al.*, 1989). The established components of the pRB pathway include the E2F transcription factors, which are involved in transcriptional control of numerous cellular genes responsible for the advances of cells through the cell cycle (Nevins, 1992; La Thangue, 1994). The pRB also interacts with certain G1 phase cyclins (Koff *et al.*, 1992; Resnitzky and Reed, 1995; Geng *et al.*, 1996). Therefore, the RB gene apparently plays a key role in cell growth regulation being involved in the major decisions during the G1 phase of the cell cycle which govern cell proliferation, quiescence and differentiation (Weinberg, 1995). Furthermore, only the underphosphorylated RB protein binds to SV40 large T antigen. Given that RB protein binding by large T antigen is probably important for the growth promoting effects of large T antigen, this suggests that the underphosphorylated RB protein is the active form of the RB protein, and the phosphorylated RB protein in S and G2 phases is inactive (Ludlow *et al.*, 1989).

It was reported that there was a striking difference in the ratio of underphosphorylated to phosphorylated pRB forms between normal fibroblasts growing exponentially and those arrested in G1 phase. More underphosphorylated pRB was observed in G1 arrested cells, suggesting the change in ratio of phosphorylated to underphosphorylated RB proteins was related to the fluctuation of cell cycle (Xu *et al.*, 1989b). Four subsequent papers have described the cell cycle-dependent phosphorylation of RB protein in detail (DeCaprio *et al.*, 1989; Buchkovich *et al.*; 1989; Chen *et al.*, 1989; Mihara *et al.*, 1989). It is now widely accepted that the product of the RB gene has a key role in the cell cycle control.

Cell proliferation depends on transcriptional activation of genes that are responsible for the onset of DNA synthesis as well as other critical events in the G1 phase of the cell cycle. As demonstrated by Pardee, transition of cells from a serum mitogens-dependent to serum mitogens-independent state is separated by a distinct time point at several hours before the onset of S phase, namely the R (restriction) point (Pardee, 1989). By passing through the R point, the cell commits itself to complete the remainder of the cell cycle through M phase. Therefore, the R point between the middle G1 and late G1 phases of the cell cycle represents a transition in the life of the cell that is as important as the G1/S boundary.

The phosphorylation status of pRB undergoes a readily distinguishable alteration at a time close to and perhaps contemporaneous with the R point transition of the cell cycle (Weinberg, 1995). During middle G1 phase, the only pRB species detected is an underphosphorylated form. When cells progress through the cell cycle, the pRB content increases gradually. However, the majority of pRB synthesized after middle G1 phase is hyperphosphorylated. In other words, pRB hyperphosphorylation occurs in late G1, preceding the G1/S boundary (Xu *et al.*, 1991a; Mittnacht *et al.*, 1994). pRB maintains this hyperphosphorylated status throughout the remainder of the cell cycle, becoming dephosphorylated only upon evolution from M/early G1 (Ludlow *et al.*, 1990; Xu *et al.*, 1991a; Mittnacht *et al.*, 1994).

The underphosphorylated form of pRB is able to form complexes with the transcription factor E2Fs or directly interact with the E2F site, and switches the E2F site from a positive to negative element in transcriptional control. The E2F site is present in the promoters of diverse cellular genes that are responsible for the advances of cells through the cell cycle, including c-myc, B-myb, cdc2, dihydrofolate reductase, thymidine kinase, and the RB as well as the E2F-1 gene itself (Chellappan *et al.*, 1991; Nevins, 1992; Weintraub *et al.*, 1992; La Thangue, 1994; Shan *et al.*, 1994; Sardet *et al.*, 1995; Shan *et al.*, 1996). Since hyperphosphorylated pRB appears to have lost the ability to interact with E2Fs, the inhibitory function of pRB on cell growth can be abrogated by hyperphosphorylation.

The timing of pRB phosphorylation led to an attractive functional model (Weinberg, 1995). This model suggests that pRB is an R point guardian. pRB exerts most of its growth inhibitory effects in the first two thirds of the G1 phase. A cell that has progressed through early and middle G1 encounters the R point gate. Should conditions be ready for advance into the remainder of the cell cycle, pRB will undergo phosphorylation and functional inactivation, causing it to open the gate and to permit the cell to proceed into late G1. Cells that lack normal pRB function for various reasons will proceed freely into late G1. Without pRB, the upstream components of the cell cycle clock that regulate pRB phosphorylation, such as cyclin D, cyclin E and their corresponding cyclin-dependent kinases (CDKs) (Kato *et al.*, 1993; Ewen *et al.*, 1993) lose much of their influences in the decision of the cell to pass through the R point gate. Taken together, pRB allows the cell cycle clock to control the expression of numerous genes that

mediate advance of the cell through a critical phase of its growth cycle being involved in the major decisions concurrent with the R point transition. Functional loss of pRB deprives the cell of this clock and thus of an important mechanism for braking cell proliferation.

Various mutations of the RB gene are known, and these are generally inactive. Mutations in RB are seen in virtually all cases of retinoblastoma; additionally, the RB gene products could potentially be inactivated by hyperphosphorylation, and by viral oncoprotein-like cellular protein binding. Although the RB gene was initially named because deletions or mutations within the gene caused the rare childhood ocular tumor, retinoblastoma, loss of pRB function is not only causally related to the retinoblastoma, but is also linked to the progression of many common human cancers. Additionally, there is growing evidence suggesting that the RB protein status is potentially a prognostic marker in urothelial carcinoma, non-small cell lung carcinoma, and perhaps also in some other types of human neoplasms (Xu, 1995).

In addition, with the revolutionary antigen retrieval technique and the available specific anti-pRB antibodies, immunohistochemistry has recently become one of the highly sensitive and reliable methods for detection of pRB inactivation in routinely processed pathological specimens (Xu, 1995). Altered pRB expression as determined by immunohistochemical analysis appears to signal a poor prognosis in a subset of human malignancies. It was initially reported that loss of functional pRB was a statistically significant negative prognostic factor in high-grade adult soft tissue sarcomas (Cance *et al.*, 1990). Subsequently, two independent studies done concurrently concluded that altered pRB expression was a prognostic factor among patients with transitional cell carcinoma of the bladder (Cordon-Cardo *et al.*, 1992; Logothetis *et al.*, 1992).

For lung cancer patients, the initial pilot studies have also been promising, implying that altered RB and p53 protein status could be a synergistic prognostic factor in early stage non-small cell lung carcinomas (Xu *et al.*, 1994a). A much worse survival pattern has been reported as well for patients with acute myelogenous leukemia who have low or absent levels of pRB protein in their peripheral blood leukemic cells (Kornblau *et al.*, 1994). Since all studies done so far to investigate association between the pRB status in human cancer and the clinical outcome of the patients have been retrospective, and the number of cases in each cohort was fairly small, definitive retrospective and prospective studies with an adequate sample size for statistical

calculations are now underway to determine whether or not loss of pRB function can be considered as a prognostic factor in clinical practice.

The most direct proof that the cloned RB gene is indeed a tumor suppressor gene comes from introduction of a cloned intact copy of the gene into cancer cells with observed tumor suppression function. A number of reports have indicated that replacement of the normal RB gene in RB-defective tumor cells from disparate types of human cancers could suppress their tumorigenic activity in nude mice (Huang *et al.*, 1988; Goodrich and Lee, 1993; Zhou *et al.*, 1994b). The tumor cell lines studied were derived from widely disparate types of human cancers such as the retinoblastoma, osteosarcoma, carcinomas of the bladder, prostate, breast and lung.

Of note, there has been a tendency in the literature to separate the inhibition of cell growth by RB replacement in RB-defective tumor cells from its tumor suppression function (Takahashi *et al.*, 1991; Chen *et al.*, 1992; Goodrich *et al.*, 1992; Zhou *et al.*, 1994b). After transient transduction with a wild-type pRB-expressing retrovirus or plasmid, as documented in several early studies, the RB-deficient retinoblastoma and osteosarcoma tumor cells in culture displayed striking changes, including cell enlargement, senescent phenotype and lower growth rate (Huang *et al.*, 1988; Templeton *et al.*, 1991). Subsequently, it was found that long-term stable clones of the RB-reconstituted tumor cells can be isolated that grew just as rapidly as the parental or matched RB^- revertant clones. The majority of RB^+ clones obtained, however, were non-tumorigenic or with significantly reduced tumorigenicity in nude mice. The mechanisms for the dissociation of suppression of tumorigenicity in nude mice from inhibition of tumor cell growth in culture by RB-replacement are unclear. It is certainly possible that RB replacement restores sensitivity to a variety of physiologic growth inhibitory signals which may be present and supplied to cells when tumorigenicity assay is done in nude mice. Such external growth inhibitory agents would be absent under regular cell culture conditions, leading to rapid cell growth (Chen *et al.*, 1992).

Although the molecular mechanism of the RB-mediated tumor suppression have remained unclear, suppression of tumorigenicity of RB^- tumor cells *in vivo* by re-expressing the wild-type pRB implies that the RB gene could be a potential therapeutic target for human cancer. In addition, recent reports suggest that RB may also play a role in elicitation of immunogenicity

of tumor cells (Lu *et al.*, 1994; Lu *et al.*, 1996), anti-angiogenesis (Dawson *et al.*, 1995) and suppression of tumor invasiveness (Li *et al.*, 1996), which make the emerging RB gene therapy even more attractive. In this regard, preclinical studies have recently demonstrated that treatment of established human xenograft tumors in nude mice by recombinant adenovirus vectors expressing either wild-type or an N-terminal truncated retinoblastoma protein resulted in regression of the treated tumors (Xu *et al.*, 1996a). In addition, a constitutively active form of the pRB protein has been tested in a rat artery model of restenosis to inhibit vascular proliferative disorders following balloon angioplasty (Chang *et al.*, 1995).

The RB gene expressing the first in-frame AUG codon-initiated RB protein is also referred to herein as the intact RB gene, the RB^{110} gene or the $p110^{RB}$ coding gene. It has also been observed that lower molecular weight (<100 kD, 98 kD, or 98-104 kD) bands of unknown origin which are immunoreactive to various anti-RB antibodies can be detected in immunoprecipitation and Western blots (Xu *et al.*, 1989b; Furukawa *et al.*, 1990; Stein *et al.*, 1990).

The RB^{110} cDNA open reading frame sequence (McGee *et al.*, 1989) contains a second in-frame AUG codon located in exon 3, at nucleotides 355-357. The deduced second AUG codon-initiated RB protein would be 98 kD, or 12 kD smaller than the $p110^{RB}$ protein. It has been proposed that the lower molecular weight bands are the underphosphorylated (98 kD) and phosphorylated (98-104 kD) RB protein translated from the second AUG codon of the RB mRNA (Xu *et al.*, 1989b), and this was later shown conclusively (Xu *et al.*, U.S. Patent 5,496,731). This protein is referred to as the $p94^{RB}$ protein.

Additional "modified" retinoblastoma genes and proteins discovered by the inventors to be useful in the practice of certain aspects of the invention are described in greater detail in the Examples below.

It has been proposed that introduction of a functional RB^{110} gene into an RB-minus tumor cell will likely "normalize" the cell. Of course, it was not expected that tumor cells which already have normal RB^{110} gene expression ("RB^{+}") would respond to RB^{110} gene therapy, because it was presumed that adding additional RB expression could not correct a non-RB

genetic defect. In fact, it has been shown that in the case of RB^+ tumor cell lines, such as the osteosarcoma cell line U-2 OS, which expresses the normal $p110^{RB}$, introduction of an extra $p110^{RB}$ coding gene did not change the neoplastic phenotype of such tumor lines (Huang *et al.*, 1988).

In the only reported exception, introduction of a $p110^{RB}$ coding vector into normal human fibroblasts, WS1, which have no known RB or any other genetic defects, led to the cessation of cell growth (Fung *et al.*, WO 91/15580, 1991). However, it is believed that these findings were misinterpreted since a plasmid, ppVUO-Neo, producing SV40 T antigen with a well-known growth-promoting effect on host cells was used improperly to provide a comparison with the effect of RB^{110} expression on cell growth of transfected WS1 fibroblasts (Fung *et al.* WO 91/15580, 1991). This view is confirmed by the extensive literature, clearly characterizing RB^+ tumor cells as "incurable" by treatment with wild-type RB^{110} gene. In addition, it is noteworthy that the WS1 cell line per se is a generally recognized non-tumorigenic human diploid fibroblast cell line with limited cell division potential in culture. Therefore, WO91/15580 simply does not provide any method for effectively treating RB^+ tumors with an RB^{110} gene. Thus, there remains a need for a broad-spectrum tumor suppressor gene for treating abnormally proliferating cells having any type of genetic defect.

b. p53

Somatic cell mutations of the p53 gene are said to be the most frequently mutated gene in human cancer (Weinberg, 1991). The normal or wild-type p53 gene is a negative regulator of cell growth, which, when damaged, favors cell transformation (Weinberg, 1991). As noted for the RB protein, the p53 expression product is found in the nucleus, where it may act in parallel with or cooperatively with $p110^{RB}$. This is suggested by a number of observations, for example, both p53 and $p110^{RB}$ proteins are targeted for binding or destruction by the oncoproteins of SV40, adenovirus and human papillomavirus. Tumor cell lines deleted for p53 have been successfully treated with wild-type p53 vector to reduce tumorigenicity (Baker *et al.*, 1990). However, the introduction of either p53 or RB^{110} into cells that have not undergone lesions at these loci does not affect cell proliferation (Marshall, 1991; Baker *et al.*, 1990; Huang *et al.*, 1988). Such experiments suggest that sensitivity of cells to the suppression of their growth by a tumor suppressor gene is dependent on the genetic alterations that have taken place in the cells.

Such a dependency would be further complicated by the observation in certain cancers that alterations in the p53 tumor suppressor or gene locus appear after mutational activation of the ras oncogene (Marshall, 1991; Fearon *et al.*, 1990a). Therefore, there remains a need for a broad-spectrum tumor suppressor gene that does not depend on the specific identification of each mutated gene causing abnormal cellular proliferation.

Of particular interest, the inventors have recently identified an N-terminal region that shares 48% identity between the RB and p53 proteins. The inventors contemplate that modification of the N-terminal region of the p53 protein may yield modified p53 proteins with beneficial tumor suppression properties, as was seen with the instant modified retinoblastoma proteins.

c. Neurofibromatosis Type 1

Neurofibromatosis type 1 or von Recklinghausen neurofibromatosis results from the inheritance of a predisposing mutant allele or from alleles created through new germline mutations (Marshall, 1991). The neurofibromatosis type 1 gene, referred to as the NF1 gene, is a relatively large locus exhibiting a mutation rate of around 10^{-4}. Defects in the NF1 gene result in a spectrum of clinical syndromes ranging from cafe-au-lait spots to neurofibromas of the skin and peripheral nerves to Schwannomas and neurofibrosarcomas. The NF1 gene encodes a protein of about 2485 amino acids that shares structural similarity with three proteins that interact with the products of the ras protooncogene (Weinberg, 1991). For example, the NF1 amino acid sequence shows sequence homology to the catalytic domain of ras GAP, a GTPase-activating protein for p21 ras (Marshall, 1991).

The role of NF1 in cell cycle regulation is apparently a complex one that is not yet fully elucidated. For example, it has been hypothesized that it is a suppressor of oncogenically activated p21 ras in yeast (Marshall, 1991 citing Ballester *et al*, 1990). On the other hand, other possible pathways for NF1 interaction are suggested by the available data (Marshall, 1991; Weinberg, 1991). At present, no attempts to treat NF1 cells with a wild-type NF1 gene have been undertaken due to the size and complexity of the NF1 locus. Therefore, it would be highly desirable to have a broad-spectrum tumor suppressor gene able to treat NF1 and any other type of cancer or tumor.

d. DCC

The multiple steps in the tumorigenesis of colon cancer are readily monitored during development by colonoscopy. The combination of colonoscopy with the biopsy of the involved tissue has uncovered a number of degenerative genetic pathways leading to the result of a malignant tumor. One well studied pathway begins with large polyps in which 60% of the cells carry a mutated, activated allele of K-ras. A majority of these tumors then proceed to the inactivation-mutation of the gene referred to as the deleted in colon carcinoma (DCC) gene, followed by the inactivation of the p53 tumor suppressor gene.

The DCC gene is a more than approximately one million base pair gene coding for a 190-kD transmembrane phosphoprotein which is hypothesized to be a receptor (Weinberg, 1991), the loss of which allows the affected cell a growth advantage. It has also been noted that the DCC has partial sequence homology to the neural cell adhesion molecule (Marshall, 1991) which might suggest a role for the DCC protogene in regulating cell to cell interactions. As can be appreciated, the large size and complexity of the DCC gene, together with the complexity of the K-ras, p53 and possibly other genes involved in colon cancer tumorigenesis demonstrates a need for a broad-spectrum tumor suppressor gene and methods of treating colon carcinoma cells which do not depend upon manipulation of the DCC gene or on the identification of other specific damaged genes in colon carcinoma cells.

2. Cytokine Genes

A number of different cytokine genes are contemplated for use in the present invention. Below is an exemplary, but in no way limiting, table of cytokine genes that could be used in certain embodiments of the present invention.

Table 1

Cytokine	Reference
human IL-1α	March *et al.*, *Nature*, 315:641, 1985
murine IL-1α	Lomedico *et al.*, *Nature*, 312:458, 1984
human IL-1β	March *et al.*, *Nature*, 315:641, 1985; Auron *et al.*, *Proc. Natl. Acad. Sci. USA*, 81:7907, 1984

Table 1 (Continued)

Cytokine	Reference
murine IL-1β	Gray, *J. Immunol.*, 137:3644, 1986; Telford, *Nucl. Acids Res.*, 14:9955, 1986
human IL-1ra	Eisenberg *et al.*, *Nature*, 343:341, 1990
human IL-2	Taniguchi *et al.*, *Nature*, 302:305, 1983; Maeda *et al.*, *Biochem. Biophys. Res. Commun.*, 115:1040, 1983
human IL-2	Taniguchi *et al.*, *Nature*, 302:305, 1983
human IL-3	Yang *et al.*, *Cell*, 47:3, 1986
murine IL-3	Yokota *et al.*, *Proc. Natl. Acad. Sci. USA*, 81:1070, 1984; Fung *et al.*, *Nature*, 307:233, 1984; Miyatake *et al.*, *Proc. Natl. Acad. Sci. USA*, 82:316, 1985
human IL-4	Yokota *et al.*, *Proc. Natl. Acad. Sci. USA*, 83:5894, 1986
murine IL-4	Norma *et al.*, *Nature*, 319:640, 1986; Lee *et al.*, *Proc. Natl. Acad. Sci. USA*, 83:2061, 1986
human IL-5	Azuma *et al.*, *Nuc. Acids Res.*, 14:9149, 1986
murine IL-5	Kinashi *et al.*, *Nature*, 324:70, 1986; Mizuta *et al.*, *Growth Factors*, 1:51, 1988
human IL-6	Hirano *et al.*, *Nature*, 324:73, 1986
murine IL-6	Van Snick *et al.*, *Eur. J. Immunol.*, 18:193, 1988
human IL-7	Goodwin *et al.*, *Proc. Natl. Acad. Sci. USA*, 86:302, 1989
murine IL-7	Namen *et al.*, *Nature*, 333:571, 1988
human IL-8	Schmid *et al.*, *J. Immunol.*, 139:250, 1987; Matsushima *et al.*, *J. Exp. Med.*, 167:1883, 1988; Lindley *et al.*, *Proc. Natl. Acad. Sci. USA*, 85:9199, 1988
human IL-9	Renauld *et al.*, *J. Immunol.*, 144:4235, 1990
murine IL-9	Renauld *et al.*, *J. Immunol.*, 144:4235, 1990
human Angiogenin	Kurachi *et al.*, *Biochemistry*, 24:5494, 1985
human GROα	Richmond *et al.*, *EMBO J.*, 7:2025, 1988
murine MIP-1α	Davatelis *et al.*, *J. Exp. Med.*, 167:1939, 1988
murine MIP-1β	Sherry *et al.*, *J. Exp. Med.*, 168:2251, 1988

Table 1 (Continued)

Cytokine	Reference
human MIF	Weiser *et al.*, *Proc. Natl. Acad. Sci. USA*, 86:7522, 1989
human G-CSF	Nagata *et al.*, *Nature*, 319:415, 1986; Souza *et al.*, *Science*, 232:61, 1986
human GM-CSF	Cantrell *et al.*, *Proc. Natl. Acad. Sci. USA*, 82:6250, 1985; Lee *et al.*, *Proc. Natl. Acad. Sci. USA*, 82:4360, 1985; Wong *et al.*, *Science*, 228:810, 1985
murine GM-CSF	Gough *et al.*, *EMBO J.*, 4:645, 1985
human M-CSF	Wong, *Science*, 235:1504, 1987; Kawasaki, *Science*, 230;291, 1985; Ladner, *EMBO J.*, 6:2693, 1987
human EGF	Smith *et al.*, *Nuc. Acids Res.*, 10:4467, 1982; Bell *et al.*, *Nucl. Acids Res.*, 14:8427, 1986
human TGF-α	Derynck *et al.*, *Cell*, 38:287, 1984
human FGF acidic	Jaye *et al.*, *Science*, 233:541, 1986; Gimenez-Gallego *et al.*, *Biochem. Biophys. Res. Commun.*, 138:611, 1986; Harper *et al.*, *Biochem.*, 25:4097, 1986
human β-ECGF	Jaye *et al.*, *Science*, 233:541, 1986
human FGF basic	Abraham *et al.*, *EMBO J.*, 5:2523, 1986; Sommer *et al.*, *Biochem. Biophys. Res. Comm.*, 144:543, 1987
murine IFN-β	Higashi *et al.*, *J. Biol. Chem.*, 258:9522, 1983; Kuga, *Nucl. Acids Res.*, 17:3291, 1989
human IFN-γ	Gray *et al.*, *Nature*, 295:503, 1982; Devos *et al.*, *Nucl. Acids Res.*, 10:2487, 1982; Rinderknecht, *J. Biol. Chem.*, 259:6790, 1984
human IGF-I	Jansen *et al.*, *Nature*, 306:609, 1983; Rotwein *et al.*, *J. Biol. Chem.*, 261:4828, 1986
human IGF-II	Bell *et al.*, *Nature*, 310:775, 1984
human β-NGF chain	Ullrich *et al.*, *Nature*, 303:821, 1983
human PDGF A chain	Betsholtz *et al.*, *Nature*, 320:695, 1986
human PDGF B chain	Johnsson *et al.*, *EMBO J.*, 3:921, 1984; Collins *et al.*, *Nature*, 316:748, 1985

Table 1 (Continued)

Cytokine	Reference
human TGF-β1	Derynck *et al.*, *Nature*, 316:701, 1985
human TNF-α	Pennica *et al.*, *Nature*, 312:724, 1984; Fransen *et al.*, *Nuc. Acids Res.*, 13:4417, 1985
human TNF-β	Gray *et al.*, *Nature*, 312:721, 1984
murine TNF-β	Gray *et al.*, *Nucl. Acids Res.*, 15:3937, 1987

D. Heterologous Genes

While tumor suppressor and cytokine genes are preferred in a number of embodiments of the present invention, in other embodiments a variety of heterologous genes are contemplated for use. Below is a list of selected cloned structural genes that could be used in the present invention. The list is not in any way meant to be interpreted as limiting, only as exemplary of the types of structural genes contemplated for use in the present invention.

Table 2

	Selected Cloned Structural Genes	
Gene	Clone Type*	Reference
activin	porcine-cDNA	Mason AJ, Nat, 318:659, 1985
adenosine deaminase	h-cDNA	Wiginton DA, PNAS, 80:7481, 1983
angiotensinogen I	r-cDNA	Ohkubo H, PNAS, 80:2196, 1983
	r-gDNA	Tanaka T, JBC, 259:8063, 1984
antithrombin III	H-cDNA	Bock SC, NAR 10:8113, 1982
	h-cDNA and gDNA	Prochownik EV, JBC, 258:8389, 1983
antitrypsin, alpha I	h-cDNA	Kurachi K, PNAS, 78:6826, 1981
	h-gDNA	Leicht M, Nat, 297:655, 1982
	RFLP	Cox DW, AJHG, 36:134S, 1984
apolipoprotein A-I	h-cDNA, h-gDNA	Shoulders CC, NAR, 10:4873, 1982
	RFLP	Karathanasis SK, Nat, 301:718, 1983
	h-gDNA	Kranthanasis SK, PNAS, 80:6147, 1983

Table 2 (Continued)

	Selected Cloned Structural Genes	
Gene	Clone Type*	Reference
apolipoprotein A-II	h-cDNA	Sharpe CR, NAR, 12:3917, 1984
	Chr	Sakaguchi, AY, AJHB, 36:207S, 1984
	h-cDNA	Knott TJ, BBRC, 120:734, 1984
apolipoprotein C-I	h-cDNA	Knott TJ, NAR, 12:3909, 1984
apolipoprotein C-II	h-cDNA	Jackson CL, PNAS, 81:2945, 1984
	h-cDNA	Mykelbost O, JBC, 249:4401, 1984
	h-cDNA	Fojo SS, PNAS, 81:6354, 1984
	RFLP	Humphries SE, C Gen, 26:389, 1984
apolipoprotein C-III	h-cDNA and gDNA	Karanthanasis SK, Nat, 304:371, 1983
	h-cDNA	Sharpe CR, NAR, 12:3917, 1984
apolipoprotein E	h-cDNA	Brewslow JL, JBC, 257:14639, 1982
atrial natriuretic factor	h-cDNA	Oikawa S, Nat, 309:724, 1984
	h-cDNA	Nakayama K, Nat, 310:699, 1984
	h-cDNA	Zivin RA, PNAS, 81:6325, 1984
	h-gDNA	Seidman CE, Sci, 226:1206, 1984
	h-gDNA	Nemer M, Nat, 312:654, 1984
	h-gDNA	Greenberg BI, Nat, 312:665, 1984
chorionic gonadotropin, alpha chain	h-cDNA	Fiddes JC, Nat, 281:351, 1981
	RFLP	Boethby M, JBC, 256:5121, 1981
chorionic gonadotropin, beta chain	h-cDNA	Fiddes JC, Nat, 286:684, 1980
	h-gDNA	Boorstein WR, Nat, 300:419, 1982
	h-gDNA	Talmadge K, Nat, 307:37, 1984
chymosin, pro (rennin)	bovine-cDNA	Harris TJR, NAR, 10:2177, 1982
complement, factor B	h-cDNA	Woods DE, PNAS, 79:5661, 1982
	h-cDNA and gDNA	Duncan R, PNAS, 80:4464, 1983

Table 2 (Continued)

	Selected Cloned Structural Genes	
Gene	Clone Type*	Reference
complement C2	h-cDNA	Bentley DR, PNAS, 81:1212, 1984
	h-gDNA (C2, C4, and B)	Carroll MC, Nat, 307:237, 1984
complement C3	m-cDNA	Domdey H, PNAS, 79:7619, 1983
	h-gDNA	Whitehead AS, PNAS, 79:5021, 1982
complement C4	h-cDNA and gDNA	Carroll MC, PNAS, 80:264, 1983
	h-cDNA	Whitehead AS, PNAS, 80:5387, 1983
complement C9	h-cDNA	DiScipio RC, PNAS, 81:7298, 1984
corticotropin releasing	sheep-cDNA	Furutani Y, Nat, 301:537, 1983
factor	h-gDNA	Shibahara S, EMBO J, 2:775, 1983
epidermal growth	m-cDNA	Gray A, Nat, 303:722, 1983
factor	m-cDNA	Scott J, Sci, 21:236, 1983
	h-gDNA	Brissenden JE, Nat, 310:781, 1984
epidermal growth	h-cDNA and Chr	Lan CR, Sci, 224:843, 1984
factor		
receptor, oncogene		
c-erb B		
epoxide dehydratase	r-cDNA	Gonzlalez FJ, JBC, 256:4697, 1981
erythropoietin	h-cDNA	Lee-Huang S, PNAS, 81:2708, 1984
esterase inhibitor, C1	h-cDNA	Stanley KK, EMBO J, 3:1429, 1984
factor VIII	h-cDNA and gDNA	Gitschier J, Nat, 312:326, 1984
	h-cDNA	Toole JJ, Nat, 312:342, 1984
factor IX, Christmas	h-cDNA	Kutachi K, PNAS, 79:6461, 1982
factor	h-cDNA	Choo KH, Nat, 299:178, 1982
	RFLP	Camerino G, PNAS, 81:498, 1984
	h-gDNA	Anson DS, EMBO J, 3:1053, 1984
factor X	h-cDNA	Leytus SP, PNAS, 81:3699, 1984
fibrinogen A alpha,	h-cDNA	Kant JA, PNAS, 80:3953, 1983

Table 2 (Continued)

	Selected Cloned Structural Genes	
Gene	Clone Type*	Reference
B beta, gamma	h-gDNA (gamma)	Fornace AJ, Sci, 224:161, 1984
	h-cDNA (alpha	Imam AMA, NAR, 11:7427, 1983
	gamma)	Fornace AJ, JBC, 259:12826, 1984
	h-gDNA (gamma)	
gastrin releasing	h-cDNA	Spindel ER, PNAS, 81:5699, 1984
peptide		
glucagon, prepro	hamster c-DNA	Bell GI, Nat, 302:716, 1983
	h-gDNA	Bell GI, Nat, 304:368, 1983
growth hormone	h-cDNA	Martial JA, Sci, 205:602, 1979
	h-gDNA	DeNoto FM, NAR, 9:3719, 1981
	GH-like gene	Owerbach, D, Sci, 209:289, 1980
growth hormone, RF,	h-cDNA	Gubler V, PNAS, 80:3411, 1983
somatocrinin	h-cDNA	Mayo KE, Nat, 306:86:1983
hemopexin	h-cDNA	Stanley KK, EMBO J, 3:1429, 1984
inhibin	porcine-cDNA	Mason AJ, Nat, 318:659, 1985
insulin, prepro	h-gDNA	Ullrich a, Sci, 209:612, 1980
insulin-like growth	h-cDNA	Jansen M, Nat, 306:609, 1983
factor I	h-cDNA	Bell GI, Nat, 310:775, 1984
	Chr	Brissenden JE, Nat, 310:781, 1984
insulin-like growth	h-cDNA	Bell GI, Nat, 310:775, 1984
factor II	h-gDNA	Dull TJ, Nat, 310:777, 1984
	Chr	Brissenden JE, Nat, 310:781, 1984
interferon, alpha	h-cDNA	Maeda S, PNAS, 77:7010, 1980
(leukocyte), multiple	h-cDNA (8 distinct)	Goeddel DV, Nat., 290:20, 1981
	h-gDNA	Lawn RM, PNAS, 78:5435, 1981
	h-gDNA	Todokoro K, EMBO J, 3:1809, 1984
	h-gDNA	Torczynski RM, PNAS, 81:6451, 1984

Table 2 (Continued)

	Selected Cloned Structural Genes	
Gene	Clone Type*	Reference
interferon, beta (fibroblast)	h-cDNA	Taniguchi T, Gene, 10:11, 1980
	h-gDNA	Lawn RM, NAR, 9:1045, 1981
	h-gDNA (related)	Sehgal P, PNAS, 80:3632, 1983
	h-gDNA (related)	Sagar AD, Sci, 223:1312, 1984
interferon, gamma (immune)	h-cDNA	Gray PW, Nat, 295:503, 1982
	h-gDNA	Gray PW, Nat, 298:859, 1982
interleukin-1	m-cDNA	Lomedico PT, Nat, 312:458, 1984
interleukin-2, T-cell growth factor	h-cDNA	Devos R, NAR, 11:4307, 1983
	h-cDNA	Taniguchi T, Nat, 302:305, 1983
	h-gDNA	Hollbrook NJ, PNAS, 81:1634, 1984
	Chr	Siegel LF, Sci, 223:175, 1984
interleukin-3	m-cDNA	Fung MC, Nat, 307:233, 1984
kininogen, two forms	bovine-cDNA	Nawa H, PNAS, 80:90, 1983
	bovine,-cDNA and gDNA	Kitamura N, Nat, 305:545, 1983
leuteinizing hormone, beta subunit	h-gDNA and Chr	Talmadge K, Nat, 207:37, 1984
leuteinizing hormone releasing hormone	h-cDNA and gDNA	Seeburg PH, Nat, 311:666, 1984
lymphotoxin	h-cDNA and gDNA	Gray PW, Nat, 312:721, 1984
mast cell growth factor	m-cDNA	Yokoya T, PNAS, 81:1070, 1984
nerve growth factor, beta subunit	m-cDNA	Scott J, Nat, 302:538, 1983
	h-gDNA	Ullrich A, Nat, 303:821, 1983
	Chr	Franke C, Sci, 222:1248, 1983
oncogene, c-sis, PGDF chain A	h-gDNA	Dalla-Favera R, Nat, 295:31, 1981
	h-cDNA	Clarke MF, Nat, 208:464, 1984

Table 2 (Continued)

	Selected Cloned Structural Genes	
Gene	Clone Type*	Reference
pancreatic polypeptide and icosapeptide	h-cDNA	Boel E, EMBO J, 3:909, 1984
parathyroid hormone,	h-cDNA	Hendy GN, PNAS, 78:7365, 1981
prepro	h-gDNA	Vasicek TJ, PNAS, 80:2127, 1983
plasminogen	h-cDNA and gDNA	Malinowski DP, Fed P, 42:1761, 1983
plasminogen activator	h-cDNA	Edlund T, PNAS, 80:349, 1983
	h-cDNA	Pennica D, Nat, 301:214, 1983
	h-gDNA	Ny T, PNAS, 81:5355, 1984
prolactin	h-cDNA	Cook NE, JBC, 256:4007, 1981
	r-gDNA	Cooke NE, Nat, 297:603, 1982
proopiomelanocortin	h-cDNA	DeBold CR, Sci, 220:721, 1983
	h-gDNA	Cochet M, Nat, 297:335, 1982
protein C	h-cDNA	Foster D, PNAS, 81:4766, 1984
prothrombin	bovine-cDNA	MacGillivray RTA, PNAS, 77:5153, 1980
relaxin	h-gDNA	Hudson P, Nat, 301:628, 1983
	h-cDNA (2 genes)	Hudson P, EMBO J, 3:2333, 1984
	Chr	Crawford, RJ, EMBO J, 3:2341, 1984
renin, prepro	h-cDNA	Imai T, PNAS, 80:7405, 1983
	h-gDNA	Hobart PM, PNAS 81:5026, 1984
	h-gDNA	Miyazaki H, PNAS, 81:5999, 1984
	Chr	Chirgwin JM, SCMG, 10:415, 1984
somatostatin	h-cDNA	Shen IP, PNAS, 79:4575, 1982
	h-gDNA and Ri-IP	Naylot SI, PNAS, 80:2686, 1983
tachykinin, prepro,	bovine-cDNA	Nawa H, Nat, 306:32, 1983
substances P & K	bovine-gDNA	Nawa H, Nat, 312:729, 1984
urokinase	h-cDNA	Verde P, PNAS, 81:4727, 1984
vasoactive intestinal peptide, prepro	h-cDNA	Itoh N, Nat, 304:547, 1983

Table 2 (Continued)

	Selected Cloned Structural Genes	
Gene	Clone Type*	Reference
vasopressin	r-cDNA	Schmale H, EMBO J, 2:763, 1983

Key to Table 2: *cDNA - complementary DNA; Chr - chromosome; gDNA - genomic DNA; RFLP - restriction fragment polymorphism; h - human; m - mouse; r - rat

E. Marker Genes

In certain aspects of the present invention, specific cells are tagged with specific genetic markers to provide information about the fate of the tagged cells. Therefore, the present invention also provides recombinant candidate screening and selection methods which are based upon whole cell assays and which, preferably, employ a reporter gene that confers on its recombinant hosts a readily detectable phenotype that emerges only under conditions where a general DNA promoter positioned upstream of the reporter gene is functional. Generally, reporter genes encode a polypeptide (marker protein) not otherwise produced by the host cell which is detectable by analysis of the cell culture, *e.g.*, by fluorometric, radioisotopic or spectrophotometric analysis of the cell culture.

In other aspects of the present invention, a genetic marker is provided which is detectable by standard genetic analysis techniques, such as DNA or RNA amplification by PCR™ or hybridization using fluorometric, radioisotopic or spectrophotometric probes.

1. Screening

Exemplary enzymes include esterases, phosphatases, proteases (tissue plasminogen activator or urokinase) and other enzymes capable of being detected by their activity, as will be known to those skilled in the art. Contemplated for use in the present invention is green fluorescent protein (GFP) as a marker for transgene expression (Chalfie *et al.*, 1994). The use of GFP does not need exogenously added substrates, only irradiation by near UV or blue light, and thus has significant potential for use in monitoring gene expression in living cells.

Other particular examples are the enzyme chloramphenicol acetyltransferase (CAT) which may be employed with a radiolabelled substrate, firefly and bacterial luciferase, and the bacterial enzymes β-galactosidase and β-glucuronidase. Other marker genes within this class are well known to those of skill in the art, and are suitable for use in the present invention.

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2. Selection

Another class of reporter genes which confer detectable characteristics on a host cell are those which encode polypeptides, generally enzymes, which render their transformants resistant against toxins. Examples of this class of reporter genes are the *neo* gene (Colberre-Garapin
10 *et al.*, 1981) which protects host cells against toxic levels of the antibiotic G418, the gene conferring streptomycin resistance (U. S. Patent No. 4,430,434), the gene conferring hygromycin B resistance (Santerre *et al.*, 1984; U. S. Patent Nos. 4,727,028, 4,960,704 and 4,559,302), a gene encoding dihydrofolate reductase, which confers resistance to methotrexate (Alt *et al.*, 1978), the enzyme HPRT, along with many others well known in the art (Kaufman, 1990).

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F. Biological Functional Equivalents

While the present invention contemplates the use of tumor suppressor proteins, exemplified by the retinoblastoma protein, which contain modifications within the N-terminal region which confer equal or greater tumor suppression activity on the resultant protein,
20 alteration of the unmodified C-terminal portion of the protein such that biological activity is maintained also falls within the scope of the present invention.

As mentioned above, modification and changes may be made in the structure of, for example, the retinoblastoma protein, and still obtain a molecule having like or otherwise
25 desirable characteristics. For example, certain amino acids may be substituted for other amino acids in a protein structure without appreciable loss of tumor suppression activity. Since it is the interactive capacity and nature of a protein that defines that protein's biological functional activity, certain amino acid sequence substitutions can be made in a protein sequence (or, of course, its underlying DNA coding sequence) and nevertheless obtain a protein with like
30 (agonistic) properties. Equally, the same considerations may be employed to create a protein or polypeptide with countervailing (*e.g.*, antagonistic) properties. It is thus contemplated by the

inventors that various changes may be made in the sequence of tumor suppressor proteins or peptides (or underlying DNA) without appreciable loss of their biological utility or activity.

In terms of functional equivalents, It is also well understood by the skilled artisan that, inherent in the definition of a biologically functional equivalent protein or peptide, is the concept that there is a limit to the number of changes that may be made within a defined portion of the molecule and still result in a molecule with an acceptable level of equivalent biological activity. Biologically functional equivalent peptides are thus defined herein as those peptides in which certain, not most or all, of the amino acids may be substituted. Of course, a plurality of distinct proteins/peptides with different substitutions may easily be made and used in accordance with the invention.

It is also well understood that where certain residues are shown to be particularly important to the biological or structural properties of a protein or peptide, *e.g.*, residues in active sites, such residues may not generally be exchanged.

Conservative substitutions well known in the art include, for example, the changes of: alanine to serine; arginine to lysine; asparagine to glutamine or histidine; aspartate to glutamate; cysteine to serine; glutamine to asparagine; glutamate to aspartate; glycine to proline; histidine to asparagine or glutamine; isoleucine to leucine or valine; leucine to valine or isoleucine; lysine to arginine, glutamine, or glutamate; methionine to leucine or isoleucine; phenylalanine to tyrosine, leucine or methionine; serine to threonine; threonine to serine; tryptophan to tyrosine; tyrosine to tryptophan or phenylalanine; and valine to isoleucine or leucine.

In making such changes, the hydropathic index of amino acids may be considered. Each amino acid has been assigned a hydropathic index on the basis of their hydrophobicity and charge characteristics, these are: isoleucine (+4.5); valine (+4.2); leucine (+3.8); phenylalanine (+2.8); cysteine/cystine (+2.5); methionine (+1.9); alanine (+1.8); glycine (-0.4); threonine (-0.7); serine (-0.8); tryptophan (-0.9); tyrosine (-1.3); proline (-1.6); histidine (-3.2); glutamate (-3.5); glutamine (-3.5); aspartate (-3.5); asparagine (-3.5); lysine (-3.9); and arginine (-4.5).

The importance of the hydropathic amino acid index in conferring interactive biological function on a protein is generally understood in the art (Kyte and Doolittle, 1982, incorporated herein by reference). It is known that certain amino acids may be substituted for other amino acids having a similar hydropathic index or score and still retain a similar biological activity. In making changes based upon the hydropathic index, the substitution of amino acids whose hydropathic indices are within ±2 is preferred, those which are within ±1 are particularly preferred, and those within ±0.5 are even more particularly preferred.

It is also understood in the art that the substitution of like amino acids can be made effectively on the basis of hydrophilicity. U.S. Patent 4,554,101, incorporated herein by reference, states that the greatest local average hydrophilicity of a protein, as governed by the hydrophilicity of its adjacent amino acids, correlates with its immunogenicity and antigenicity, i.e. with a biological property of the protein. use this shorter portion for non-immunological stuff It is understood that an amino acid can be substituted for another having a similar hydrophilicity value and still obtain a biologically equivalent, and in particular, an immunologically equivalent protein.

As detailed in U.S. Patent 4,554,101, the following hydrophilicity values have been assigned to amino acid residues: arginine (+3.0); lysine (+3.0); aspartate (+3.0 ± 1); glutamate (+3.0 ± 1); serine (+0.3); asparagine (+0.2); glutamine (+0.2); glycine (0); threonine (-0.4); proline (-0.5 ± 1); alanine (-0.5); histidine (-0.5); cysteine (-1.0); methionine (-1.3); valine (-1.5); leucine (-1.8); isoleucine (-1.8); tyrosine (-2.3); phenylalanine (-2.5); tryptophan (-3.4).

In making changes based upon similar hydrophilicity values, the substitution of amino acids whose hydrophilicity values are within ±2 is preferred, those which are within ±1 are particularly preferred, and those within ±0.5 are even more particularly preferred.

While discussion has focused on functionally equivalent polypeptides arising from amino acid changes, it will be appreciated that these changes may be effected by alteration of the encoding DNA; taking into consideration also that the genetic code is degenerate and that two or more codons may code for the same amino acid. A table of amino acids and their codons is

presented below for use in such embodiments, as well as for other uses, such as in the design of probes and primers and the like.

Table 3 - Preferred Human DNA Codons

Amino Acids			Codons					
Alanine	Ala	A	GCC	GCT	GCA	GCG		
Cysteine	Cys	C	TGC	TGT				
Aspartic acid	Asp	D	GAC	GAT				
Glutamic acid	Glu	E	GAG	GAA				
Phenylalanine	Phe	F	TTC	TTT				
Glycine	Gly	G	GGC	GGG	GGA	GGT		
Histidine	His	H	CAC	CAT				
Isoleucine	Ile	I	ATC	ATT	ATA			
Lysine	Lys	K	AAG	AAA				
Leucine	Leu	L	CTG	CTC	TTG	CTT	CTA	TTA
Methionine	Met	M	ATG					
Asparagine	Asn	N	AAC	AAT				
Proline	Pro	P	CCC	CCT	CCA	CCG		
Glutamine	Gln	Q	CAG	CAA				
Arginine	Arg	R	CGC	AGG	CGG	AGA	CGA	CGT
Serine	Ser	S	AGC	TCC	TCT	AGT	TCA	TCG
Threonine	Thr	T	ACC	ACA	ACT	ACG		
Valine	Val	V	GTG	GTC	GTT	GTA		
Tryptophan	Trp	W	TGG					
Tyrosine	Tyr	Y	TAC	TAT				

Codon prevalence shown as decreasing from left (most prevalent) to right (least prevalent). Underlined codons are those used less than 5 times per one thousand codons.

Table 4 - Preferred Human RNA Codons

Amino Acids			Codons					
Alanine	Ala	A	GCC	GCU	GCA	GCG		
Cysteine	Cys	C	UGC	UGU				
Aspartic acid	Asp	D	GAC	GAU				
Glutamic acid	Glu	E	GAG	GAA				
Phenylalanine	Phe	F	UUC	UUU				
Glycine	Gly	G	GGC	GGG	GGA	GGU		
Histidine	His	H	CAC	CAU				
Isoleucine	Ile	I	AUC	AUU	AUA			
Lysine	Lys	K	AAG	AAA				
Leucine	Leu	L	CUG	CUC	UUG	CUU	CUA	UUA
Methionine	Met	M	AUG					
Asparagine	Asn	N	AAC	AAU				
Proline	Pro	P	CCC	CCU	CCA	CCG		
Glutamine	Gln	Q	CAG	CAA				
Arginine	Arg	R	CGC	AGG	CGG	AGA	CGA	CGU
Serine	Ser	S	AGC	UCC	UCU	AGU	UCA	UCG
Threonine	Thr	T	ACC	ACA	ACU	ACG		
Valine	Val	V	GUG	GUC	GUU	GUA		
Tryptophan	Trp	W	UGG					
Tyrosine	Tyr	Y	UAC	UAU				

Codon prevalence shown as decreasing from left (most prevalent) to right (least prevalent). Underlined codons are those used less than 5 times per one thousand codons.

G. Mutagenesis

Mutagenesis may be performed in accordance with any of the techniques known in the art such as and not limited to synthesizing an oligonucleotide having one or more mutations within the sequence of a particular tumor suppressor or cytokine protein. In particular, site-specific mutagenesis is a technique useful in the preparation of individual peptides, or biologically

functional equivalent proteins or peptides, through specific mutagenesis of the underlying DNA. The technique further provides a ready ability to prepare and test sequence variants, for example, incorporating one or more of the foregoing considerations, by introducing one or more nucleotide sequence changes into the DNA.

Site-specific mutagenesis allows the production of mutants through the use of specific oligonucleotide sequences which encode the DNA sequence of the desired mutation, as well as a sufficient number of adjacent nucleotides, to provide a primer sequence of sufficient size and sequence complexity to form a stable duplex on both sides of the deletion junction being traversed. Typically, a primer of about 17 to about 75 nucleotides or more in length is preferred, with about 10 to about 25 or more residues on both sides of the junction of the sequence being altered.

In general, the technique of site-specific mutagenesis is well known in the art, as exemplified by various publications. As will be appreciated, the technique typically employs a phage vector which exists in both a single stranded and double stranded form. Typical vectors useful in site-directed mutagenesis include vectors such as the M13 phage. These phage are readily commercially available and their use is generally well known to those skilled in the art. Double stranded plasmids are also routinely employed in site directed mutagenesis which eliminates the step of transferring the gene of interest from a plasmid to a phage.

In general, site-directed mutagenesis in accordance herewith is performed by first obtaining a single-stranded vector or melting apart of two strands of a double stranded vector which includes within its sequence a DNA sequence which encodes the desired peptide. An oligonucleotide primer bearing the desired mutated sequence is prepared, generally synthetically. This primer is then annealed with the single-stranded vector, and subjected to DNA polymerizing enzymes such as *E. coli* polymerase I Klenow fragment, in order to complete the synthesis of the mutation-bearing strand. Thus, a heteroduplex is formed wherein one strand encodes the original non-mutated sequence and the second strand bears the desired mutation. This heteroduplex vector is then used to transform or transfect appropriate cells, such as *E. coli* cells, and clones are selected which include recombinant vectors bearing the mutated sequence arrangement. A

genetic selection scheme was devised by Kunkel *et al.*, (1987) to enrich for clones incorporating the mutagenic oligonucleotide.

Alternatively, the use of PCR™ with commercially available thermostable enzymes such as *Taq* polymerase may be used to incorporate a mutagenic oligonucleotide primer into an amplified DNA fragment that can then be cloned into an appropriate cloning or expression vector. The PCR™-mediated mutagenesis procedures of Tomic *et al.*, (1990) and Upender *et al.*, (1995) provide two examples of such protocols. A PCR™ employing a thermostable ligase in addition to a thermostable polymerase may also be used to incorporate a phosphorylated mutagenic oligonucleotide into an amplified DNA fragment that may then be cloned into an appropriate cloning or expression vector. The mutagenesis procedure described by Michael (1994) provides an example of one such protocol.

The preparation of sequence variants of the selected peptide-encoding DNA segments using site-directed mutagenesis is provided as a means of producing potentially useful species and is not meant to be limiting as there are other ways in which sequence variants of peptides and the DNA sequences encoding them may be obtained. For example, recombinant vectors encoding the desired peptide sequence may be treated with mutagenic agents, such as hydroxylamine, to obtain sequence variants.

As used herein, the term "oligonucleotide directed mutagenesis procedure" refers to template-dependent processes and vector-mediated propagation which result in an increase in the concentration of a specific nucleic acid molecule relative to its initial concentration, or in an increase in the concentration of a detectable signal, such as amplification. As used herein, the term "oligonucleotide directed mutagenesis procedure" is intended to refer to a process that involves the template-dependent extension of a primer molecule. The term template dependent process refers to nucleic acid synthesis of an RNA or a DNA molecule wherein the sequence of the newly synthesized strand of nucleic acid is dictated by the well-known rules of complementary base pairing (Watson *et al.*, 1987). Typically, vector mediated methodologies involve the introduction of the nucleic acid fragment into a DNA or RNA vector, the clonal amplification of the vector, and the recovery of the amplified nucleic acid fragment. Examples of

such methodologies are provided by U.S. Patent 4,237,224, specifically incorporated herein by reference in its entirety.

H. Pharmaceutically Acceptable Compositions and Routes of Administration

Where clinical applications are contemplated, it will be necessary to prepare pharmaceutical compositions of the tetracycline-regulated vectors, recombinant viruses and cells in a form appropriate for the intended application. Generally, this will entail preparing compositions that are essentially free of pyrogens, as well as other impurities that could be harmful to humans or animals.

One will generally desire to employ appropriate salts and buffers to render nucleic acids, viruses or cells suitable for introduction into a patient. Aqueous compositions of the present invention comprise an effective amount of nucleic acids, viruses or cells, dissolved or dispersed in a pharmaceutically acceptable carrier or aqueous medium, and preferably encapsulated. The phrase "pharmaceutically or pharmacologically acceptable" refer to molecular entities and compositions that do not produce adverse, allergic, or other untoward reactions when administered to an animal or a human. As used herein, "pharmaceutically acceptable carrier" includes any and all solvents, dispersion media, coatings, antibacterial and antifungal agents, isotonic and absorption delaying agents and the like. The use of such media and agents for pharmaceutically active substances is well know in the art. Except insofar as any conventional media or agent is incompatible with the vectors or cells of the present invention, its use in therapeutic compositions is contemplated. Supplementary active ingredients, such as other anti-cancer agents, can also be incorporated into the compositions.

Solutions of the active ingredients as free base or pharmacologically acceptable salts can be prepared in water suitably mixed with surfactant, such as hydroxypropylcellulose. Dispersions also can be prepared in glycerol, liquid polyethylene glycols, mixtures thereof and in oils. Under ordinary conditions of storage and use, these preparations contain a preservative to prevent growth of microorganisms. Intravenous vehicles include fluid and nutrient replenishers. Preservatives include antimicrobial agents, anti-oxidants, chelating agents and inert gases. The pH and exact concentration of the various components in the pharmaceutical are adjusted according to well-known parameters.

An effective amount of the viruses or cells is determined based on the intended goal. The term "unit dose" refers to a physically discrete unit suitable for use in a subject, each unit containing a predetermined quantity of the therapeutic composition calculated to produce the desired response in association with its administration, *i.e.*, the appropriate route and treatment regimen. The quantity to be administered, both according to number of treatments and unit dose, depends on the subject to be treated, the state of the subject, and the protection desired. Precise amounts of the therapeutic composition also depend on the judgment of the practitioner and are peculiar to each individual.

1. Parenteral Administration

The active compounds of the present invention will often be formulated for parenteral administration, *e.g.*, formulated for injection *via* the intravenous, intramuscular, sub-cutaneous, intratumoral, peritumoral or even intraperitoneal routes. The preparation of an aqueous composition that contains a second agent(s) as active ingredients will be known to those of skill in the art in light of the present disclosure. Typically, such compositions can be prepared as injectables, either as liquid solutions or suspensions; solid forms suitable for using to prepare solutions or suspensions upon the addition of a liquid prior to injection can also be prepared; and the preparations can also be emulsified.

Solutions of the active compounds as free base or pharmacologically acceptable salts can be prepared in water suitably mixed with a surfactant, such as hydroxypropylcellulose. Dispersions can also be prepared in glycerol, liquid polyethylene glycols, and mixtures thereof and in oils. Under ordinary conditions of storage and use, these preparations contain a preservative to prevent the growth of microorganisms.

The pharmaceutical forms suitable for injectable use include sterile aqueous solutions or dispersions; formulations including sesame oil, peanut oil or aqueous propylene glycol; and sterile powders for the extemporaneous preparation of sterile injectable solutions or dispersions. In all cases the form must be sterile and must be fluid to the extent that easy syringability exists. It must be stable under the conditions of manufacture and storage and must be preserved against the contaminating action of microorganisms, such as bacteria and fungi.

The active compounds may be formulated into a composition in a neutral or salt form. Pharmaceutically acceptable salts, include the acid addition salts (formed with the free amino groups of the protein) and which are formed with inorganic acids such as, for example, hydrochloric or phosphoric acids, or such organic acids as acetic, oxalic, tartaric, mandelic, and the like. Salts formed with the free carboxyl groups can also be derived from inorganic bases such as, for example, sodium, potassium, ammonium, calcium, or ferric hydroxides, and such organic bases as isopropylamine, trimethylamine, histidine, procaine and the like.

The carrier can also be a solvent or dispersion medium containing, for example, water, ethanol, polyol (for example, glycerol, propylene glycol, and liquid polyethylene glycol, and the like), suitable mixtures thereof, and vegetable oils. The proper fluidity can be maintained, for example, by the use of a coating, such as lecithin, by the maintenance of the required particle size in the case of dispersion and by the use of surfactants. The prevention of the action of microorganisms can be brought about by various antibacterial ad antifungal agents, for example, parabens, chlorobutanol, phenol, sorbic acid, thimerosal, and the like. In many cases, it will be preferable to include isotonic agents, for example, sugars or sodium chloride. Prolonged absorption of the injectable compositions can be brought about by the use in the compositions of agents delaying absorption, for example, aluminum monostearate and gelatin.

Sterile injectable solutions are prepared by incorporating the active compounds in the required amount in the appropriate solvent with various of the other ingredients enumerated above, as required, followed by filtered sterilization. Generally, dispersions are prepared by incorporating the various sterilized active ingredients into a sterile vehicle which contains the basic dispersion medium and the required other ingredients from those enumerated above. In the case of sterile powders for the preparation of sterile injectable solutions, the particular methods of preparation are vacuum-drying and freeze-drying techniques which yield a powder of the active ingredient plus any additional desired ingredient from a previously sterile-filtered solution thereof.

For parenteral administration in an aqueous solution, for example, the solution should be suitably buffered if necessary and the liquid diluent first rendered isotonic with sufficient saline

or glucose. These particular aqueous solutions are especially suitable for intravenous, intramuscular, subcutaneous, intratumoral, peritumoral and intraperitoneal administration. In this connection, sterile aqueous media which can be employed will be known to those of skill in the art in light of the present disclosure. For example, one dosage could be dissolved in 1 ml of isotonic NaCl solution and either added to 1000 ml of hypodermoclysis fluid or injected at the proposed site of infusion, (see for example, "Remington's Pharmaceutical Sciences" 15th Edition, pages 1035-1038 and 1570-1580). Some variation in dosage will necessarily occur depending on the condition of the subject being treated. The person responsible for administration will, in any event, determine the appropriate dose for the individual subject.

2. Other Routes of Administration

In addition to the compounds formulated for parenteral administration, such as intravenous or intramuscular injection, other pharmaceutically acceptable forms include, *e.g.*, tablets or other solids for oral administration; time release capsules; and any other form currently used, including cremes, lotions, mouthwashes, inhalants and the like.

The expression vectors and delivery vehicles of the present invention may include classic pharmaceutical preparations. Administration of these compositions according to the present invention will be *via* any common route so long as the target tissue is available *via* that route. This includes oral, nasal, buccal, rectal, vaginal or topical. Alternatively, administration may be by orthotopic, intradermal, subcutaneous, intramuscular, intraperitoneal or intravenous injection. The injection can be general, regional, local or direct injection, for example, of a tumor. Also contemplated is injection of a resected tumor bed, and continuous perfusion *via* catheter. Such compositions would normally be administered as pharmaceutically acceptable compositions, described *supra*.

The vectors of the present invention are advantageously administered in the form of injectable compositions either as liquid solutions or suspensions; solid forms suitable for solution in, or suspension in, liquid prior to injection also may be prepared. These preparations also may be emulsified. A typical compositions for such purposes comprises a 50 mg or up to about 100 mg of human serum albumin per milliliter of phosphate buffered saline. Other pharmaceutically acceptable carriers include aqueous solutions, non-toxic excipients, including salts, preservatives,

buffers and the like. Examples of non-aqueous solvents are propylene glycol, polyethylene glycol, vegetable oil and injectable organic esters, such as theyloleate. Aqueous carriers include water, alcoholic/aqueous solutions, saline solutions, parenteral vehicles such as sodium chloride, Ringer's dextrose, *etc.* Intravenous vehicles include fluid and nutrient replenishers. Preservatives include antimicrobial agents, anti-oxidants, chelating agents and inert gases. The pH and exact concentration of the various components in the pharmaceutical are adjusted according to well known parameters.

Additional formulations are suitable for oral administration. Oral formulations include such typical excipients as, for example, pharmaceutical grades of mannitol, lactose, starch, magnesium stearate, sodium saccharine, cellulose, magnesium carbonate and the like. The compositions take the form of solutions, suspensions, tablets, pills, capsules, sustained release formulations or powders. When the route is topical, the form may be a cream, ointment, salve or spray.

An effective amount of the therapeutic agent is determined based on the intended goal. The term "unit dose" refers to a physically discrete unit suitable for use in a subject, each unit containing a predetermined quantity of the therapeutic composition calculated to produce the desired response in association with its administration, *i.e.*, the appropriate route and treatment regimen. The quantity to be administered, both according to number of treatments and unit dose, depends on the subject to be treated, the state of the subject and the protection desired. Precise amounts of the therapeutic composition also depend on the judgment of the practitioner and are peculiar to each individual.

In certain cases, the therapeutic formulations of the invention could also be prepared in forms suitable for topical administration, such as in cremes and lotions. These forms may be used for treating skin-associated diseases, such as various sarcomas.

Upon formulation, solutions will be administered in a manner compatible with the dosage formulation and in such amount as is therapeutically effective. The formulations are easily administered in a variety of dosage forms, such as the type of injectable solutions described above, with even drug release capsules and the like being employable.

I. Chemotherapeutic Agents

The methods of the present invention may be combined with any other methods generally employed in the treatment of the particular disease or disorder that the patient exhibits. For example, in connection with the treatment of solid tumors, the methods of the present invention may be used in combination with classical approaches, such as surgery, radiotherapy and the like. So long as a particular therapeutic approach is not known to be detrimental in itself, or counteracts the effectiveness of the tumor suppressor therapy, its combination with the present invention is contemplated. When one or more agents are used in combination with cytokine gene therapy and/or tumor suppressor gene therapy, there is no requirement for the combined results to be additive of the effects observed when each treatment is conducted separately, although this is evidently desirable, and there is no particular requirement for the combined treatment to exhibit synergistic effects, although this is certainly possible and advantageous.

In terms of surgery, any surgical intervention may be practiced in combination with the present invention. In connection with radiotherapy, any mechanism for inducing DNA damage locally within tumor cells is contemplated, such as γ-irradiation, X-rays, UV-irradiation, microwaves and even electronic emissions and the like. The directed delivery of radioisotopes to tumor cells is also contemplated, and this may be used in connection with a targeting antibody or other targeting means. Cytokine therapy also has proven to be an effective partner for combined therapeutic regimens. Various cytokines may be employed in such combined approaches. Examples of cytokines include IL-1α IL-1β, IL-2, IL-3, IL-4, IL-5, IL-6, IL-7, IL-8, IL-9, IL-10, IL-11, IL-12, IL-13, TGF-β, GM-CSF, M-CSF, G-CSF, TNFα, TNFβ, LAF, TCGF, BCGF, TRF, BAF, BDG, MP, LIF, OSM, TMF, PDGF, IFN-α, IFN-β, IFN-γ. Cytokines are administered according to standard regimens, consistent with clinical indications such as the condition of the patient and relative toxicity of the cytokine.

Compositions of the present invention can have an effective amount of a0n engineered virus or cell for therapeutic administration in combination with an effective amount of a compound (second agent) that is a chemotherapeutic agent as exemplified below. Such compositions will generally be dissolved or dispersed in a pharmaceutically acceptable carrier or aqueous medium. A wide variety of chemotherapeutic agents may be used in combination with

the therapeutic genes of the present invention. These can be, for example, agents that directly cross-link DNA, agents that intercalate into DNA, and agents that lead to chromosomal and mitotic aberrations by affecting nucleic acid synthesis.

Irrespective of the mechanisms by which the enhanced tumor destruction is achieved, the combined treatment aspects of the present invention have evident utility in the effective treatment of disease. To use certain compositions of the present invention in combination with the administration of a chemotherapeutic agent, for example, one would simply administer to an animal at least a first tumor suppressor as disclosed herein in combination with the chemotherapeutic agent in a manner effective to result in their combined anti-tumor actions within the animal. These agents would therefore be provided in an amount effective and for a period of time effective to result in their combined presence and their combined actions in the tumor environment. To achieve this goal, the tumor suppressor and chemotherapeutic agents may be administered to the animal simultaneously, either in a single composition or as two distinct compositions using different administration routes.

Alternatively, the tumor suppressor treatment may precede or follow the chemotherapeutic agent treatment by intervals ranging from minutes to weeks. In embodiments where the chemotherapeutic factor and tumor suppressor are applied separately to the animal, one would generally ensure that a significant period of time did not expire between the time of each delivery, such that the chemotherapeutic agent and tumor suppressor composition would still be able to exert an advantageously combined effect on the tumor. In such instances, it is contemplated that one would contact the tumor with both agents within about 5 minutes to about one week of each other and, more preferably, within about 12-72 hours of each other, with a delay time of only about 12-48 hours being most preferred. In some situations, it may be desirable to extend the time period for treatment significantly, where several days (2, 3, 4, 5, 6 or 7) or even several weeks (1, 2, 3, 4, 5, 6, 7 or 8) lapse between the respective administrations. It also is conceivable that more than one administrations of either the tumor suppressor or the chemotherapeutic agent will be desired. To achieve tumor regression, both agents are delivered in a combined amount effective to inhibit its growth, irrespective of the times for administration.

A variety of chemotherapeutic agents are intended to be of use in the combined treatment methods disclosed herein. Chemotherapeutic agents contemplated as exemplary include, *e.g.*, etoposide (VP-16), adriamycin, 5-fluorouracil (5FU), camptothecin, actinomycin-D, mitomycin C, cisplatin (CDDP) and even hydrogen peroxide. In certain embodiments, the use of etoposide is effective in regression of tumor in size when administered in combination with the compositions of the present invention.

As will be understood by those of ordinary skill in the art, the appropriate doses of chemotherapeutic agents will be generally around those already employed in clinical therapies wherein the chemotherapeutics are administered alone or in combination with other chemotherapeutics. By way of example only, agents such as cisplatin, and other DNA alkylating may be used. Cisplatin has been widely used to treat cancer, with efficacious doses used in clinical applications of 20 mg/m^2 for 5 days every three weeks for a total of three courses. Cisplatin is not absorbed orally and must therefore be delivered *via* injection intravenously, subcutaneously, intratumorally or intraperitoneally.

Agents that directly cross-link nucleic acids, specifically DNA, are envisaged and are shown herein, to eventuate DNA damage leading to a synergistic antineoplastic combination. Agents such as cisplatin, and other DNA alkylating agents may be used.

Further useful agents include compounds that interfere with DNA replication, mitosis and chromosomal segregation. Such chemotherapeutic compounds include adriamycin, also known as doxorubicin, etoposide, verapamil, podophyllotoxin, and the like. Widely used in a clinical setting for the treatment of neoplasms, these compounds are administered through bolus injections intravenously at doses ranging from 25-75 mg/m^2 at 21 day intervals for adriamycin, to 35-50 mg/m^2 for etoposide intravenously or double the intravenous dose orally.

Agents that disrupt the synthesis and fidelity of polynucleotide precursors may also be used. Particularly useful are agents that have undergone extensive testing and are readily available. As such, agents such as 5-fluorouracil (5-FU) are preferentially used by neoplastic tissue, making this agent particularly useful for targeting to neoplastic cells. Although quite

toxic, 5-FU, is applicable in a wide range of carriers, including topical, however intravenous administration with doses ranging from 3 to 15 mg/kg/day being commonly used.

Plant alkaloids such as taxol are also contemplated for use in certain aspects of the present invention. Taxol is an experimental antimitotic agent, isolated from the bark of the ash tree, *Taxus brevifolia*. It binds to tubulin (at a site distinct from that used by the vinca alkaloids) and promotes the assembly of microtubules. Taxol is currently being evaluated clinically; it has activity against malignant melanoma and carcinoma of the ovary. Maximal doses are 30 mg/m^2 per day for 5 days or 210 to 250 mg/m^2 given once every 3 weeks. Of course, all of these dosages are exemplary, and any dosage in-between these points is also expected to be of use in the invention.

Exemplary chemotherapeutic agents that are useful in connection with combined therapy are listed in Table 5. Each of the agents listed therein are exemplary and by no means limiting. The skilled artisan is directed to "Remington's Pharmaceutical Sciences" 15th Edition, chapter 33, in particular pages 624-652. Some variation in dosage will necessarily occur depending on the condition of the subject being treated. The person responsible for administration will, in any event, determine the appropriate dose for the individual subject. Moreover, for human administration, preparations should meet sterility, pyrogenicity, general safety and purity standards as required by FDA Office of Biologics standards.

Table 5

Chemotherapeutic Agents Useful In Neoplastic Disease

Class	Type Of Agent	Nonproprietary Names (Other Names)	Disease
	Nitrogen Mustards	Mechlorethamine (HN_2)	Hodgkin's disease, non-Hodgkin's lymphomas
		Cyclophosphamide Ifosfamide	Acute and chronic lymphocytic leukemias, Hodgkin's disease, non-Hodgkin's lymphomas, multiple myeloma, neuroblastoma, breast, ovary, lung, Wilms' tumor, cervix, testis, soft-tissue sarcomas
		Melphalan (L-sarcolysin)	Multiple myeloma, breast, ovary

Table 5 (Continued)

Class	Type Of Agent	Nonproprietary Names (Other Names)	Diseas
		Chlorambucil	Chronic lymphocytic leukemia, primary macroglobulinemia, Hodgkin's disease, non-Hodgkin's lymphomas
Alkylating Agents	Ethylenimenes and Methylmelamines	Hexamethylmelamine	Ovary
		Thiotepa	Bladder, breast, ovary
	Alkyl Sulfonates	Busulfan	Chronic granulocytic leukemia
		Carmustine (BCNU)	Hodgkin's disease, non-Hodgkin's lymphomas, primary brain tumors, multiple myeloma, malignant melanoma
	Nitrosoureas	Lomustine (CCNU)	Hodgkin's disease, non-Hodgkin's lymphomas, primary brain tumors, small-cell lung
		Semustine (methyl-CCNU)	Primary brain tumors, stomach, colon
		Streptozocin (streptozotocin)	Malignant pancreatic insulinoma, malignant carcinoid
	Triazines	Dacarbazine (DTIC; dimethyltriazenoimidazolecarboxamide)	Malignant melanoma, Hodgkin's disease, soft-tissue sarcomas
	Folic Acid Analogs	Methotrexate (amethopterin)	Acute lymphocytic leukemia, choriocarcinoma, mycosis fungoides, breast, head and neck, lung, osteogenic sarcoma
	Pyrimidine Analogs	Fluouracil (5-fluorouracil; 5-FU)	Breast, colon, stomach, pancreas, ovary, head and neck, urinary bladder, premalignant skin lesions (topical)
		Floxuridine (fluorodeoxyuridine; FUdR)	
Antimetabolites		Cytarabine (cytosine arabinoside)	Acute granulocytic and acute lymphocytic leukemias
		Mercaptopurine (6-mercaptopurine; 6-MP)	Acute lymphocytic, acute granulocytic and chronic granulocytic leukemias

Table 5 (Continued)

Class	Type Of Agent	Nonproprietary Names (Other Names)	Disease
Natural Products	Purine Analogs and Related Inhibitors	Thioguanine (6-thioguanine; TG)	Acute granulocytic, acute lymphocytic and chronic granulocytic leukemias
		Pentostatin (2-deoxycoformycin)	Hairy cell leukemia, mycosis fungoides, chronic lymphocytic leukemia
	Vinca Alkaloids	Vinblastine (VLB)	Hodgkin's disease, non-Hodgkin's lymphomas, breast, testis
		Vincristine	Acute lymphocytic leukemia, neuroblastoma, Wilms' tumor, rhabdomyosarcoma, Hodgkin's disease, non-Hodgkin's lymphomas, small-cell lung
	Epipodophyllotoxins	Etoposide (VP16)	Testis, small-cell lung and other lung, breast, Hodgkin's disease, non-Hodgkin's lymphomas, acute granulocytic leukemia, Kaposi's sarcoma
		Tertiposide	
	Antibiotics	Dactinomycin (actinomycin D)	Choriocarcinoma, Wilms' tumor, rhabdomyosarcoma, testis, Kaposi's sarcoma
		Daunorubicin (daunomycin; rubidomycin)	Acute granulocytic and acute lymphocytic leukemias
		Doxorubicin	Soft-tissue, osteogenic and other sarcomas; Hodgkin's disease, non-Hodgkin's lymphomas, acute leukemias, breast, genitourinary, thyroid, lung, stomach, neuroblastoma
		Bleomycin	Testis, head and neck, skin, esophagus, lung and genitourinary tract; Hodgkin's disease, non-Hodgkin's lymphomas
Natural Products, continued	Antibiotics, continued	Plicamycin (mithramycin)	Testis, malignant hypercalcemia
		Mitomycin (mitomycin C)	Stomach, cervix, colon, breast, pancreas, bladder, head and neck
	Enzymes	L-Asparaginase	Acute lymphocytic leukemia

Table 5 (Continued)

Class	Type Of Agent	Nonproprietary Names (Other Names)	Disease
	Biological Response Modifiers	Interferon alfa	Hairy cell leukemia., Kaposi's sarcoma, melanoma, carcinoid, renal cell, ovary, bladder, non-Hodgkin's lymphomas, mycosis fungoides, multiple myeloma, chronic granulocytic leukemia
	Platinum Coordination Complexes	Cisplatin (*cis*-DDP) Carboplatin	Testis, ovary, bladder, head and neck, lung, thyroid, cervix, endometrium, neuroblastoma, osteogenic sarcoma
	Anthracenedione	Mitoxantrone	Acute granulocytic leukemia, breast
Miscellaneous Agents	Substituted Urea	Hydroxyurea	Chronic granulocytic leukemia, polycythemia vera, essental thrombocytosis, malignant melanoma
	Methyl Hydrazine Derivative	Procarbazine (N-methylhydrazine, MIH)	Hodgkin's disease
	Adrenocortical Suppressant	Mitotane (*o,p'*-DDD) Aminoglutethimide	Adrenal cortex Breast
	Adrenocorticosteroids	Prednisone (several other equivalent preparations available)	Acute and chronic lymphocytic leukemias, non-Hodgkin's lymphomas, Hodgkin's disease, breast
	Progestins	Hydroxyprogesterone caproate Medroxyprogesterone acetate Megestrol acetate	Endometrium, breast
Hormones and Antagonists	Estrogens	Diethylstilbestrol Ethinyl estradiol (other preparations available)	Breast, prostate
	Antiestrogen	Tamoxifen	Breast
	Androgens	Testosterone propionate Fluoxymesterone (other preparations available)	Breast
	Antiandrogen	Flutamide	Prostate

Table 5 (Continued)

Class	Type Of Agent	Nonproprietary Names (Other Names)	Disease
	Gonadotropin-releasing hormone analog	Leuprolide	Prostate

J. Protein Purification

Certain aspects of the present invention concern the purification, and in particular embodiments, the substantial purification, of an encoded protein or peptide. The term "purified protein or peptide " as used herein, is intended to refer to a composition, isolatable from other components, wherein the protein or peptide is purified to any degree relative to its naturally-obtainable state. A purified protein or peptide therefore also refers to a protein or peptide, free from the environment in which it may naturally occur.

Generally, "purified" will refer to a protein or peptide composition that has been subjected to fractionation to remove various other components, and which composition substantially retains its expressed biological activity. Where the term "substantially purified" is used, this designation will refer to a composition in which the protein or peptide forms the major component of the composition, such as constituting about 50% or more of the proteins in the composition.

Various methods for quantifying the degree of purification of the protein or peptide will be known to those of skill in the art in light of the present disclosure. These include, for example, determining the specific activity of an active fraction, or assessing the number of polypeptides within a fraction by SDS/PAGE analysis. A preferred method for assessing the purity of a fraction is to calculate the specific activity of the fraction, to compare it to the specific activity of the initial extract, and to thus calculate the degree of purity, herein assessed by a "-fold purification number". The actual units used to represent the amount of activity will, of course, be dependent upon the particular assay technique chosen to follow the purification and whether or not the expressed protein or peptide exhibits a detectable activity.

Various techniques suitable for use in protein purification will be well known to those of skill in the art. These include, for example, precipitation with ammonium sulphate, PEG, antibodies and the like or by heat denaturation, followed by centrifugation; chromatography steps such as ion exchange, gel filtration, reverse phase, hydroxylapatite and affinity chromatography; isoelectric focusing; gel electrophoresis; and combinations of such and other techniques. As is generally known in the art, it is believed that the order of conducting the various purification steps may be changed, or that certain steps may be omitted, and still result in a suitable method for the preparation of a substantially purified protein or peptide.

There is no general requirement that the protein or peptide always be provided in their most purified state. Indeed, it is contemplated that less substantially purified products will have utility in certain embodiments. Partial purification may be accomplished by using fewer purification steps in combination, or by utilizing different forms of the same general purification scheme. For example, it is appreciated that a cation-exchange column chromatography performed utilizing an HPLC apparatus will generally result in a greater -fold purification than the same technique utilizing a low pressure chromatography system. Methods exhibiting a lower degree of relative purification may have advantages in total recovery of protein product, or in maintaining the activity of an expressed protein.

It is known that the migration of a polypeptide can vary, sometimes significantly, with different conditions of SDS/PAGE (Capaldi *et al.*, 1977). It will therefore be appreciated that under differing electrophoresis conditions, the apparent molecular weights of purified or partially purified expression products may vary.

High Performance Liquid Chromatography (HPLC) is characterized by a very rapid separation with extraordinary resolution of peaks. This is achieved by the use of very fine particles and high pressure to maintain and adequate flow rate. Separation can be accomplished in a matter of minutes, or a most an hour. Moreover, only a very small volume of the sample is needed because the particles are so small and close-packed that the void volume is a very small fraction of the bed volume. Also, the concentration of the sample need not be very great because the bands are so narrow that there is very little dilution of the sample.

Gel chromatography, or molecular sieve chromatography, is a special type of partition chromatography that is based on molecular size. The theory behind gel chromatography is that the column, which is prepared with tiny particles of an inert substance that contain small pores, separates larger molecules from smaller molecules as they pass through or around the pores, depending on their size. As long as the material of which the particles are made does not adsorb the molecules, the sole factor determining rate of flow is the size. Hence, molecules are eluted from the column in decreasing size, so long as the shape is relatively constant. Gel chromatography is unsurpassed for separating molecules of different size because separation is independent of all other factors such as pH, ionic strength, temperature, *etc.* There also is virtually no adsorption, less zone spreading and the elution volume is related in a simple matter to molecular weight.

Affinity chromatography is a chromatographic procedure that relies on the specific affinity between a substance to be isolated and a molecule that it can specifically bind to. This is a receptor-ligand type interaction. The column material is synthesized by covalently coupling one of the binding partners to an insoluble matrix. The column material is then able to specifically adsorb the substance from the solution. Elution occurs by changing the conditions to those in which binding will not occur (alter pH, ionic strength, temperature, *etc.*).

A particular type of affinity chromatography useful in the purification of carbohydrate containing compounds is lectin affinity chromatography. Lectins are a class of substances that bind to a variety of polysaccharides and glycoproteins. Lectins are usually coupled to agarose by cyanogen bromide. Conconavalin A coupled to Sepharose was the first material of this sort to be used and has been widely used in the isolation of polysaccharides and glycoproteins other lectins that have been include lentil lectin, wheat germ agglutinin which has been useful in the purification of N-acetyl glucosaminyl residues and *Helix pomatia* lectin. Lectins themselves are purified using affinity chromatography with carbohydrate ligands. Lactose has been used to purify lectins from castor bean and peanuts; maltose has been useful in extracting lectins from lentils and jack bean; N-acetyl-D galactosamine is used for purifying lectins from soybean; N-acetyl glucosaminyl binds to lectins from wheat germ; D-galactosamine has been used in obtaining lectins from clams and L-fucose will bind to lectins from lotus.

The matrix should be a substance that itself does not adsorb molecules to any significant extent and that has a broad range of chemical, physical and thermal stability. The ligand should be coupled in such a way as to not affect its binding properties. The ligand should also provide relatively tight binding. And it should be possible to elute the substance without destroying the sample or the ligand. One of the most common forms of affinity chromatography is immunoaffinity chromatography.

K. Use of Cells in Bioreactors

The ability to produce biologically active polypeptides is increasingly important to the pharmaceutical industry. The present invention discloses compositions and methods for the efficient regulated expression of selected genes in cells, allowing for the production of possibly deleterious proteins *in vitro* from previously refractory cell types.

Over the last decade, advances in biotechnology have led to the production of important proteins and factors from bacteria, yeast, insect cells and from mammalian cell culture. Mammalian cultures have advantages over cultures derived from the less advanced lifeforms in their ability to post-translationally process complex protein structures such as disulfide-dependent folding and glycosylation. Indeed, mammalian cell culture is now the preferred source of a number of important proteins for use in human and animal medicine, especially those which are relatively large, complex or glycosylated.

Development of mammalian cell culture for production of pharmaceuticals has been greatly aided by the development in molecular biology of techniques for design and construction of vector systems highly efficient in mammalian cell cultures, a battery of useful selection markers, gene amplification schemes and a more comprehensive understanding of the biochemical and cellular mechanisms involved in procuring the final biologically-active molecule from the introduced vector.

However, the traditional selection of cell types for expressing heterologous proteins has generally been limited to the more "common" cell types such as CHO cells, BHK cells, C127 cells and myeloma cells. In many cases, these cell types were selected because there was a great deal of preexisting literature on the cell type or the cell was simply being carried in the

laboratory at the time the effort was made to express a peptide product. Frequently, factors which affect the downstream (*e.g.*, beyond the T-75 flask) side of manufacturing scale-up were not considered before selecting the cell line as the host for the expression system.

Aspects of the present invention take advantage of the biochemical and cellular capacities of mammalian cells as well as of recently available bioreactor technology. Growing cells according to the present invention in a bioreactor allows for large scale production and secretion of complex, fully biologically-active polypeptides into the growth media. In particular embodiments, by designing a defined media with low contents of complex proteins and using a scheme of timed-stimulation of the secretion into the media for increased titer, the purification strategy can be greatly simplified, thus lowering production cost.

1. Anchorage-dependent and non-anchorage-dependent cultures.

Animal and human cells can be propagated *in vitro* in two modes: as non-anchorage dependent cells growing freely in suspension throughout the bulk of the culture; or as anchorage-dependent cells requiring attachment to a solid substrate for their propagation (*i.e.*, a monolayer type of cell growth).

Non-anchorage dependent or suspension cultures from continuous established cell lines are the most widely used means of large scale production of cells and cell products. Large scale suspension culture based on microbial (bacterial and yeast) fermentation technology has clear advantages for the manufacturing of mammalian cell products. The processes are relatively straightforward to operate and scale up. Homogeneous conditions can be provided in the reactor which allows for precise monitoring and control of temperature, dissolved oxygen, and pH, and ensure that representative samples of the culture can be taken.

However, suspension cultured cells cannot always be used in the production of biologicals. Suspension cultures are still considered to have tumorigenic potential and thus their use as substrates for production put limits on the use of the resulting products in human and veterinary applications (Petricciani, 1985; Larsson and Litwin, 1987). Viruses propagated in suspension cultures as opposed to anchorage-dependent cultures can sometimes cause rapid changes in viral markers, leading to reduced immunogenicity (Bahnemann, 1980). Finally,

sometimes even recombinant cell lines can secrete considerably higher amounts of products when propagated as anchorage-dependent cultures as compared with the same cell line in suspension (Nilsson and Mosbach, 1987). For these reasons, different types of anchorage-dependent cells are used extensively in the production of different biological products.

The current invention includes cells which are anchorage-dependent of nature. Anchorage-dependent cells, when grown in suspension, will attach to each other and grow in clumps, eventually suffocating cells in the inner core of each clump as they reach a size that leaves the core cells unsustainable by the culture conditions. Therefore, an efficient means of large-scale culture of anchorage-dependent cells is also provided in order to effectively take advantage of the cells' capacity to secrete heterologous proteins.

2. Reactors and processes for suspension.

Large scale suspension culture of mammalian cultures in stirred tanks is contemplated. The instrumentation and controls for bioreactors have been adapted, along with the design of the fermentors, from related microbial applications. However, acknowledging the increased demand for contamination control in the slower growing mammalian cultures, improved aseptic designs have been implemented, improving dependability of these reactors. Instrumentation and controls include agitation, temperature, dissolved oxygen, and pH controls. More advanced probes and autoanalyzers for on-line and off-line measurements of turbidity (a function of particles present), capacitance (a function of viable cells present), glucose/lactate, carbonate/bicarbonate and carbon dioxide are also available. Maximum cell densities obtainable in suspension cultures are relatively low at about 2-4 $\times 10^6$ cells/ml of medium (which is less than 1 mg dry cell weight per ml), well below the numbers achieved in microbial fermentation.

Two suspension culture reactor designs are most widely used in the industry due to their simplicity and robustness of operation - the stirred reactor and the airlift reactor. The stirred reactor design has successfully been used on a scale of 8000 liter capacity for the production of interferon (Phillips *et al.*, 1985; Mizrahi, 1983). Cells are grown in a stainless steel tank with a height-to-diameter ratio of 1:1 to 3:1. The culture is usually mixed with one or more agitators, based on bladed disks or marine propeller patterns. Agitator systems offering less shear forces than blades have been described. Agitation may be driven either directly or indirectly by

magnetically coupled drives. Indirect drives reduce the risk of microbial contamination through seals on stirrer shafts.

The airlift reactor, also initially described for microbial fermentation and later adapted for mammalian culture, relies on a gas stream to both mix and oxygenate the culture. The gas stream enters a riser section of the reactor and drives circulation. Gas disengages at the culture surface, causing denser liquid free of gas bubbles to travel downward in the downcomer section of the reactor. The main advantage of this design is the simplicity and lack of need for mechanical mixing. Typically, the height-to-diameter ratio is 10:1. The airlift reactor scales up relatively readily, has good mass transfer of gasses and generates relatively low shear forces.

Most large-scale suspension cultures are operated as batch or fed-batch processes because they are the most straightforward to operate and scale up. However, continuous processes based on chemostat or perfusion principles are available.

A batch process is a closed system in which a typical growth profile is seen. A lag phase is followed by exponential, stationary and decline phases. In such a system, the environment is continuously changing as nutrients are depleted and metabolites accumulate. This makes analysis of factors influencing cell growth and productivity, and hence optimization of the process, a complex task. Productivity of a batch process may be increased by controlled feeding of key nutrients to prolong the growth cycle. Such a fed-batch process is still a closed system because cells, products and waste products are not removed.

In what is still a closed system, perfusion of fresh medium through the culture can be achieved by retaining the cells with a fine mesh spin filter and spinning to prevent clogging. Spin filter cultures can produce cell densities of approximately 5×10^7 cells/ml. A true open system and the most basic perfusion process is the chemostat in which there is an inflow of medium and an outflow of cells and products. Culture medium is fed to the reactor at a predetermined and constant rate which maintains the dilution rate of the culture at a value less than the maximum specific growth rate of the cells (to prevent washout of the cell mass from the reactor). Culture fluid containing cells, cell products and byproducts is removed at the same rate. These perfused systems are not in commercial use for production from mammalian cell culture.

3. Non-perfused attachment systems.

Traditionally, anchorage-dependent cell cultures are propagated on the bottom of small glass or plastic vessels. The restricted surface-to-volume ratio offered by classical and traditional techniques, suitable for the laboratory scale, has created a bottleneck in the production of cells and cell products on a large scale. To provide systems that offer large accessible surfaces for cell growth in small culture volume, a number of techniques have been proposed: the roller bottle system, the stack plates propagator, the spiral film bottles, the hollow fiber system, the packed bed, the plate exchanger system, and the membrane tubing reel. Since these systems are non-homogeneous in their nature, and are sometimes based on multiple processes, they can sometimes have limited potential for scale-up, difficulties in taking cell samples, limited potential for measuring and controlling the system and difficulty in maintaining homogeneous environmental conditions throughout the culture.

A commonly used process of these systems is the roller bottle. Being little more than a large, differently shaped T-flask, simplicity of the system makes it very dependable and, hence, attractive. Fully automated robots are available that can handle thousands of roller bottles per day, thus eliminating the risk of contamination and inconsistency associated with the otherwise required intense human handling. With frequent media changes, roller bottle cultures can achieve cell densities of close to 0.5×10^6 cells/cm^2 (corresponding to 10^9 cells/bottle or 10^7 cells/ml of culture media).

4. Cultures on microcarriers

van Wezel (1967) developed the concept of the microcarrier culturing systems. In this system, cells are propagated on the surface of small solid particles suspended in the growth medium by slow agitation. Cells attach to the microcarriers and grow gradually to confluency of the microcarrier surface. In fact, this large scale culture system upgrades the attachment dependent culture from a single disc process to a unit process in which both monolayer and suspension culture have been brought together. Thus, combining the necessary surface for the cells to grow with the advantages of the homogeneous suspension culture increases production.

The advantages of microcarrier cultures over most other anchorage-dependent, large-scale cultivation methods are several fold. First, microcarrier cultures offer a high surface-to-volume ratio (variable by changing the carrier concentration) which leads to high cell density yields and a potential for obtaining highly concentrated cell products. Cell yields are up to 1-2 x 10^7 cells/ml when cultures are propagated in a perfused reactor mode. Second, cells can be propagated in one unit process vessels instead of using many small low-productivity vessels (*i.e.*, flasks or dishes). This results in far better utilization and a considerable saving of culture medium. Moreover, propagation in a single reactor leads to reduction in need for facility space and in the number of handling steps required per cell, thus reducing labor cost and risk of contamination.

Third, the well-mixed and homogeneous microcarrier suspension culture makes it possible to monitor and control environmental conditions (*e.g.*, pH, pO_2, and concentration of medium components), thus leading to more reproducible cell propagation and product recovery. Fourth, it is possible to take a representative sample for microscopic observation, chemical testing, or enumeration. Fifth, since microcarriers settle out of suspension easily, use of a fed-batch process or harvesting of cells can be done relatively easily. Sixth, the mode of the anchorage-dependent culture propagation on the microcarriers makes it possible to use this system for other cellular manipulations, such as cell transfer without the use of proteolytic enzymes, cocultivation of cells, transplantation into animals, and perfusion of the culture using decanters, columns, fluidized beds, or hollow fibers for microcarrier retainment. Seventh, microcarrier cultures are relatively easily scaled up using conventional equipment used for cultivation of microbial and animal cells in suspension.

5. Microencapsulation of mammalian cells

One method which has shown to be particularly useful for culturing mammalian cells is microencapsulation. The mammalian cells are retained inside a semipermeable hydrogel membrane. A porous membrane is formed around the cells permitting the exchange of nutrients, gases, and metabolic products with the bulk medium surrounding the capsule. Several methods have been developed that are gentle, rapid and non-toxic and where the resulting membrane is sufficiently porous and strong to sustain the growing cell mass throughout the term of the culture. These methods are all based on soluble alginate gelled by droplet contact with a

calcium-containing solution. Lim (1982) describes cells concentrated in an approximately 1% solution of sodium alginate which are forced through a small orifice, forming droplets, and breaking free into an approximately 1% calcium chloride solution. The droplets are then cast in a layer of polyamino acid that ionically bonds to the surface alginate. Finally the alginate is reliquefied by treating the droplet in a chelating agent to remove the calcium ions. Other methods use cells in a calcium solution to be dropped into a alginate solution, thus creating a hollow alginate sphere. A similar approach involves cells in a chitosan solution dropped into alginate, also creating hollow spheres.

Microencapsulated cells are easily propagated in stirred tank reactors and, with beads sizes in the range of 150-1500 mm in diameter, are easily retained in a perfused reactor using a fine-meshed screen. The ratio of capsule volume to total media volume can kept from as dense as 1:2 to 1:10. With intracapsular cell densities of up to 10^8, the effective cell density in the culture is $1\text{-}5 \times 10^7$.

The advantages of microencapsulation over other processes include the protection from the deleterious effects of shear stresses which occur from sparging and agitation, the ability to easily retain beads for the purpose of using perfused systems, scale up is relatively straightforward and the ability to use the beads for implantation.

6. Perfused attachment systems

Perfusion refers to continuous flow at a steady rate, through or over a population of cells (of a physiological nutrient solution). It implies the retention of the cells within the culture unit as opposed to continuous-flow culture which washes the cells out with the withdrawn media (*e.g.*, chemostat). The idea of perfusion has been known since the beginning of the century, and has been applied to keep small pieces of tissue viable for extended microscopic observation. The technique was initiated to mimic the cells milieu *in vivo* where cells are continuously supplied with blood, lymph, or other body fluids. Without perfusion, cells in culture go through alternating phases of being fed and starved, thus limiting full expression of their growth and metabolic potential. The current use of perfused culture is to grow cells at high densities (*i.e.*, $0.1\text{-}5 \times 10^8$ cells/ml). In order to increase densities beyond $2\text{-}4 \times 10^6$ cells/ml (or 2×10^5 cells/cm^2), the medium has to be constantly replaced with a fresh supply in order to make up for

nutritional deficiencies and to remove toxic products. Perfusion allows for a far better control of the culture environment (pH, pO_2, nutrient levels, *etc.*) and is a means of significantly increasing the utilization of the surface area within a culture for cell attachment.

Microcarrier and microencapsulated cultures are readily adapted to perfused reactors but, as noted above, these culture methods lack the capacity to meet the demand for cell densities above 10^8 cells/ml. Such densities will provide for the advantage of high product titer in the medium (facilitating downstream processing), a smaller culture system (lowering facility needs), and a better medium utilization (yielding savings in serum and other expensive additives). Supporting cells at high density requires efficient perfusion techniques to prevent the development of non-homogeneity.

The cells of the present invention may, irrespective of the culture method chosen, be used in protein production and as cells for *in vitro* cellular assays and screens as part of drug development protocols.

L. Kits

All the essential materials and reagents required for the various aspects of the present invention may be assembled together in a kit. When the components of the kit are provided in one or more liquid solutions, the liquid solution preferably is an aqueous solution, with a sterile aqueous solution being particularly preferred.

For *in vivo* use, the instant compositions may be formulated into a single or separate pharmaceutically acceptable syringeable composition. In this case, the container means may itself be an inhalant, syringe, pipette, eye dropper, or other such like apparatus, from which the formulation may be applied to an infected area of the body, such as the lungs, injected into an animal, or even applied to and mixed with the other components of the kit.

The components of the kit may also be provided in dried or lyophilized forms. When reagents or components are provided as a dried form, reconstitution generally is by the addition of a suitable solvent. It is envisioned that the solvent also may be provided in another container

means. The kits of the invention may also include an instruction sheet defining administration of the gene therapy and/or the chemotherapeutic drug.

The kits of the present invention also will typically include a means for containing the vials in close confinement for commercial sale such as, *e.g.*, injection or blow-molded plastic containers into which the desired vials are retained. Irrespective of the number or type of containers, the kits of the invention also may comprise, or be packaged with, an instrument for assisting with the injection/administration or placement of the ultimate complex composition within the body of an animal. Such an instrument may be an inhalant, syringe, pipette, forceps, measured spoon, eye dropper or any such medically approved delivery vehicle. Additionally, instructions for use of the kit components is typically included.

The following examples are included to demonstrate preferred embodiments of the invention. It should be appreciated by those of skill in the art that the techniques disclosed in the examples which follow represent techniques discovered by the inventor to function well in the practice of the invention, and thus can be considered to constitute preferred modes for its practice. However, those of skill in the art should, in light of the present disclosure, appreciate that many changes can be made in the specific embodiments which are disclosed and still obtain a like or similar result without departing from the spirit and scope of the invention.

EXAMPLE 1

Modification of the CMV Promoter/Enhancer Controlling Expression of the VP16 Transactivating Domain in the Tetracycline-Responsive Gene Expression System

The original tetracycline repressor/operator-based regulatory system consists of two plasmids, pUHD15-1 and pUHC13-3 (U. S. Patent No. 5,464,758, incorporated in its entirety herein by reference; Gossen and Bujard 1992). pUHC13-3 is a tetracycline (Tc; tet) sensitive expression vector containing a hybrid minimal human CMV promoter, in which tet operator sequences had been inserted upstream of the TATA box. pUHD15-1 contains sequences encoding a tetracycline responsive transactivator (tTA), with expression driven by a wild-type CMV promoter. In transient experiments using this system, the inventors found that efficiently reversible transgene expression was observed in many tumor cell lines studied. However,

attempts to isolate long-term clones expressing the reporter gene in a tetracycline-responsive manner were unsuccessful. This was most likely caused by the high intracellular levels of the tTA transactivator, whose expression was driven by the strong CMV promoter/enhancer sequence in the plasmid pUHD15-1. The tTA transactivator contains the VP-16 activating domain, which is known to have squelching effects on cell growth (Gill and Ptashne, 1988).

Therefore, to resolve this problem and to further improve the system, the tTA expression cassette was first modified by replacing the strong CMVp enhancer (Boshart *et al.*, 1985) in the original pUHD15-1 plasmid with a pair of 19 bp imperfect direct repeat sequence (a portion of the CMVp enhancer; SEQ ID NO:7). The modification of the hCMV promoter/enhancer was done by removal of a portion of the 5' enhancer sequences from the hCMV promoter.

Three pairs of oligonucleotide primers were designed based on the published sequence of the hCMV promoter (Boshart *et al.*, 1985). A *Xho*I and an *Eco*RI restriction enzyme site (underlined) was added to the 5' end of each sense and the anti-sense oligo, respectively. The sense oligos are: 5'-CCGCTCGAGCAATGGGCGTGATAGCGG-3' (OMCMVs1; SEQ ID NO:8); 5'-CCGCTCGAGCACCAAAATCAACGGGA-3' (OMCMVs2; SEQ ID NO:9) and 5'-CCGCTCGAGCAACTCCGCCCCATTGAC-3' (OMCMVs3; SEQ ID NO:10), respectively, and they shared the same anti-sense primer, 5'-TAGACATATGAATTCGCGGCC-3' (OMCMVas; SEQ ID NO:11).

The template used in PCR™ amplification was plasmid pUHD15-1. PCR™ amplification with primer pairs of OMCMVs1 + OMCMVas; OMCMVs2 + OMCMVas and OMCMVs3 + OMCMVas, generated three shorter versions of CMV promoter with lengths of 282bp (namely mhCMVp1), 203bp (mhCMVp2) and 168bp (mhCMVp3) respectively. The purified shortened CMV promoter/enhancer fragments were double digested with *Xho*I and *Eco*RI, and inserted into pUHD15-1 to replace the original hCMV promoter. This produced three new tTA expressing plasmids, namely pmCMV1-tTA, pmCMV2-tTA and pmCMV3-tTA.

To determine the relative strength of these promoters, the tTA in these newly constructed plasmids, as well as plasmid pUHD15-1, was replaced by a chloramphenicol acetyltransferase (CAT) gene from plasmid pRc/CMV-CAT (Invitrogen, San Diego, CA), thus generating four

CAT expression plasmids, pmCMV1-CAT, pmCMV2-CAT, pmCMV3-CAT and pCMV-CAT. In these plasmids, CAT expression is driven by mhCMVp1, mhCMVp2, mhCMVp3 and the full-length hCMVp, respectively. To evaluate the relative activity of the modified CMV promoters, the CAT expression plasmids were introduced into three cell lines, the tumor cell lines 5637 and Saos2, and the embryonal kidney cell line 293, *via* the Lipofectin method (Life Technologies, Gaithersburg, MD). Forty-eight hours after transfection, cell lysates were prepared and CAT activity was measured by a CAT FLASH assay kit from Stratagene (Stratagene, La Jolla, CA).

As shown in FIG. 1, after enhancer sequences were partially removed, the activity of the promoter was dramatically reduced in all three transfected cell lines. FIG. 1 is a graphical representation of the CAT activity in the 5637 and Saos-2 cell lines. The more enhancer sequences that were deleted, the weaker was the promoter that remained. The order of promoter activity from strongest to weakest is hCMV, mhCMVp1, mhCMVp2 and mhCMVp3. The activity of mhCMVp1 is 17.7% of the full-length hCMV promoter, while the mhCMVp3 activity is only 3.3% of the hCMV promoter in 5637 cells (FIG. 1). After comparing the relative promoter activity of the modified promoters, mhCMVp1 was chosen for the modified tetracycline regulatable gene expression system. mhCMVp1 showed optimal tetracycline-controlled transactivator (tTA) expression with no squelching effects on host cell growth (FIG. 2), an important characteristic for potential use in human gene therapy.

The advantages of this modified tetracycline-regulated system also include suitability for use in gene therapy and the single-plasmid tetracycline-responsive mammalian gene expression system is readily convertible to tetracycline-controlled adenovirus and retrovirus vectors. The system provides reliable vectors for transcriptionally regulatable therapeutic gene expression because of lower constitutive levels of the tTA trans-activator, which eliminates the squelching effects of the tTA on host cell growth, and further reduces the leakiness of the original system.

EXAMPLE 2

Construction of Single Plasmid, Tetracycline-Regulated Vector

A single plasmid vector named EC1214A was constructed. This plasmid contains: 1) the modified tetracycline-responsive transactivator (tTA) expression cassette to eliminate the squelching effects of tTA on host cell growth; 2) the tTA-dependent promoter from plasmid pUHC13-3; 3) a generic intron sequence; 4) a multiple cloning site downstream of the promoter and intron; and 5) a neo^R expression cassette to allow G418 selection.

Plasmid pMLSIS.CAT (Choi *et al.*, 1991) contains an generic intron sequence which consists of a portion of the 5'-untranslated leader from the adenovirus-major-late region, which contains part of the first exon of the tripartite and the first intervening sequence, as well as a synthetic splice donor/acceptor sequence derived from an IgG variable region. A pair of oligonucleotides, 5'-CTAGAATTCGCTGTCTGCG-3' (SEQ ID NO:12) and 5'-GCTCTAGATGCAGTTGGACCTGGGAG-3' (SEQ ID NO:13), flanking the intron sequence in plasmid pMLSIS.CAT and containing an *Eco*RI and *Xba*I site, respectively (underlined), were synthesized. After amplification by PCR™, the intron fragment was digested with *Eco*RI and *Xba*I, and inserted into the corresponding enzyme sites in plasmid pUHD15-1.

Subsequently, a small DNA fragment containing *Cla*I, *Hin*dIII, *Eco*RV, *Eco*RI, *Pst*I, *Sma*I and *Bam*HI cloning sites (obtained from plasmid pBluescriptSK) was inserted into the new plasmid downstream of the intron to produce an expression vector containing the hCMV promoter, a generic intron, multiple cloning sites and a polyadenylation signal from the SV40 virus. This intermediate vector was given the name of pCMV-G. The SV40 polyadenylation signal of pCMV-G was then replaced by a HSV thymidine kinase (TK) gene polyadenylation signal sequence to generate a plasmid, named pCMV*-G-TKpA.

Plasmid pRc/CMV (Invitrogen, San Diego, CA) was double digested with restriction enzymes *Nru*I and *Xba*I. The 5' overhang from the *Xba*I digest was filled in by Klenow fragment of DNA polymerase (Life Technologies, Gaithersburg, MD), and the blunt-ended insert was ligated to a DNA fragment containing mhCMV1-tTA obtained from plasmid pmCMV1-tTA (Example 1). The new plasmid was named pmCMV1-tTA.neo.

Finally, a DNA fragment containing the tTA-dependent promoter, the generic intron and the TK polyadenylation signal was isolated from plasmid pCMV*-G-TKpA, and inserted into the *Bgl*II site of plasmid pmCMV1-tTA.neo to produce a vector named EC1214A, which carries both the tTA expression cassette and the tTA-dependent promoter as well as a selection marker, the neomycin resistance gene.

EXAMPLE 3

Construction of a Single Plasmid Tetracycline Positively-Induced (Tet-on) Vector

The original tetracycline repressor/operator-based tet-on system also consists of two plasmids, pUHD17-1neo (or pUHD172-1neo) and pUHC13-3 (Gossen *et al.*, 1995). pUHC13-3 is a tetracycline sensitive expression vector containing a hybrid minimal human CMV promoter, in which tet operator sequences had been inserted upstream of the TATA box. pUHD17-1neo or pUHD172-1neo contains sequences encoding a reverse tetracycline responsive transactivator (rtTA), with expression driven by a wild-type CMV promoter. In transient experiments using this system, it was found that efficiently reversible transgene expression was observed in many tumor cell lines studied. As opposed to the original tetracycline system, expression is turned on in the presence of tetracycline or a tetracycline analog, such as doxycycline, while expression is turned off in the absence of tetracycline. However, the rtTA transactivator contains the VP-16 activating domain, which is known to have squelching effects on cell growth (Gill and Ptashne, 1988).

Therefore, to resolve this problem and to further improve the system, the rtTA expression cassette was first modified by replacing the strong CMVp enhancer (Boshart *et al.*, 1985) in the pUHD17-1neo or pUHD172-1neo plasmid with a pair of 19 bp imperfect direct repeat sequence (SEQ ID NO:7). The modification of the hCMV promoter/enhancer was done by removal of a portion of the 5' enhancer sequences from the hCMV promoter (Example 1). The new rtTA expressing plasmid was named pmCMV1-rtTA.

A single plasmid vector named EC1214B was constructed using pmCMV1-rtTA. This plasmid contains: 1) the modified reverse tetracycline-responsive transactivator (rtTA)

expression cassette to eliminate the squelching effects of rtTA on host cell growth; 2) the rtTA-dependent promoter from plasmid pUHC13-3; 3) a generic intron sequence; 4) a multiple cloning site downstream of the promoter and intron; and 5) a neo^R expression cassette to allow G418 selection. The construction was performed as outlined in Example 2.

EXAMPLE 4

Construction of Retinoblastoma (RB) and p53 Tetracycline-Controlled Vectors

A. Construction of Inducible pRB^{110} Expression Vector

To construct an inducible pRB^{110} expression plasmid, plasmid F7 (Takahashi *et al.*, 1991) or p4.95BT (Friend *et al.*, 1987), containing the full-length RB^{110} gene cDNA, was digested with the restriction enzymes *Acy*I at nucleotide -322 and *Sca*I at +3230 (the A of the second in-frame ATG start codon was designated nucleotide +19). The 5' overhangs generated by the *Acy*I digest were treated with *E. coli* DNA polymerase I in the presence of all four dNTPs to generate blunt ends. *Bam*HI linkers were ligated onto the fragment, and the fragment was then digested with *Bam*HI to remove excess linkers and generate *Bam*HI ends (Maniatis *et al.*, 1989; Ausubel *et al.*, 1992). The resultant RB cDNA fragment of 3552 bp was inserted into the unique *Bam*HI site of EC1214A to generate pCMV*-tTA-RB^{110}.

B. Construction of Inducible pRB^{94} Expression Vector

It is known that the primary sequence surrounding the AUG codon GCC($^{A}_{G}$)CCAUGG (SEQ ID NO:29) is the optimal context for initiation of translation in higher eukaryotes (Kozak, 1991). A surprising realization is that, although nearly all vertebrate mRNAs have features that ensure the fidelity of initiation, many mRNAs that encode critical regulatory proteins do not appear to be designed for efficient translation (Kozak, 1991). In reviewing the RB cDNA sequence, it was found that the AUG start codon for both the full length pRB^{110} and the N-terminal truncated pRB^{94} are in a suboptimal context for initiation of translation in higher eukaryotes. For example, there is an out-of-frame AUG codon at the nucleotide -5 position (the A of the ATG start codon for the pRB^{94} cDNA is designated nucleotide +1), and the leading sequence of the ATG codon for pRB^{94} is suboptimal as compared to the consensus initiator context shown above. To improve the translation efficiency of the pRB^{94} cDNA, site-directed

mutagenesis was used to optimize the DNA sequence upstream of the second internal in-frame ATG codon of RB^{94} for optimal translational initiation.

The modified 5'-RB^{94} cDNA fragment was obtained by PCR™ using plasmid F7 carrying the full-length RB^{110} cDNA as the template. The sense primer used for the PCR™ reaction (5'-CCCAAGCTT*GCCGCC*ATGTCGTTCACTTTTAC-3'; SEQ ID NO:14) contained a *Hin*dIII restriction site (underlined) and a Kozak cassette (italics; Kozak, 1987). The antisense primer 5'-GTCCAAGAGAATTCATAAAAGG-3' (OMRbAS300; SEQ ID NO:15) overlapped with the *Eco*RI site (underlined) at nucleotide +900 of the RB cDNA (the A of the first in-frame ATG is designated as position +1). The PCR™ product was digested with *Hin*dIII and *Eco*RI, then ligated with a DNA fragment containing the 3'-RB cDNA fragment between *Eco*RI (position +900) and *Bam*HI (+3548) isolated from plasmid F7. The entire RB^{94} cDNA fragment was inserted into the *Hin*dIII and *Bam*HI sites of EC1214A to produce the inducible pRB^{94} expression plasmid, pCMV*-tTA-RB^{94}.

C. Construction of Inducible p53 Expression Vector

A plasmid, pC53-SN3 (Baker *et al.*, 1990), containing the full length p53 gene cDNA was digested with *Bam*HI, and the fragment containing the full length p53 gene was inserted into the unique *Bam*HI site of EC1214A to generate pCMV*-tTA-p53.

EXAMPLE 5

Preparation of Long-Term Tumor Cell Clones with Tetracycline-Regulated pRB110, pRB94 or p53 Expression

The modified, single-plasmid tetracycline-responsive mammalian gene expression system has been used to obtain various stable tumor cell lines in which expression of the wild-type or the N-terminal truncated retinoblastoma (RB) tumor suppressor gene, or the p53 tumor suppressor gene can be reversibly turned on and off without detectable leakage.

A. Cell Culture

A breast carcinoma cell line, MDA-468 (HTB132) was obtained from ATCC and cultured in Leibovitz's L-15 (Life Technologies, Gaithersburg, MD) with 10% FBS (Life

Technologies, Gaithersburg, MD). An osteosarcoma cell line, Saos2 was cultured in medium McCoy's 5A (Life Technologies, Gaithersburg, MD) with 15% FBS (Zhou *et al.*, 1994b). A bladder carcinoma cell line, 5637 (HTB9) obtained from ATCC was cultured with RPMI 1640 medium (Life Technologies, Gaithersburg, MD) containing 10% FBS. All cell culture media were supplemented with 0.5% penicillin/streptomycin. Saos2 and 5367 cells were incubated at 37°C in a 5% CO_2 incubator, while MDA-468 cells were cultured at 37°C without CO_2.

B. Stable Transfection

Tumor cells were transfected with the pRB^{110} and pRB^{94} expression plasmids, pCMV*-tTA-RB^{110} and pCMV*-tTA-RB^{94} *via* the Lipofectin method according to the manufacturer's instruction manual (Life Technologies, Gaithersburg, MD). During transfection and the subsequent procedures except where specified, 0.5 μg/ml of tetracycline (Sigma, St. Louis, MO) was added to the transfection and culture media. Forty-eight hours after transfection, G418 (Life Technologies, Gaithersburg, MD.) was added to the culture media at a concentration of 300 μg/l. Two to three weeks later, single colonies were isolated by cloning rings. A duplicate culture was made for each isolated colony. While the original clone was kept in media containing 0.5 μg/ml tetracycline, the duplicate clone was cultured in the absence of tetracycline. The latter was immunochemically stained with a specific anti-RB antibody, RB-WL-1 (Xu *et al.*, 1989a). The matched RB-positive clones were subsequently maintained in medium containing tetracycline and G418 and expended for further analyses.

C. Transient Transfection

Tumor cells were seeded into 60-mm culture dishes or onto sterile coverslips at concentrations that would reach about 40% confluent next day. Twenty hours later, proper amount of plasmid DNA was mixed with Lipofectin reagent in Opti-MEM medium according to the manufacture's instruction manual (Life Technologies, Gaithersburg, MD). Cells were overlaid with the DNA-Lipofectin complex and incubated in a CO_2 incubator at 37°C overnight. Next day, fresh medium was added to replace the DNA-Lipofectin. Twenty-four or forty-eight hours later, cells were fixed for immunochemical staining or lysed for preparation of cell lysates.

D. Immunocytochemical Staining f RB Protein

Immunocytochemical staining was performed as described previously (Xu *et al.*, 1989a). For detection of RB expression, cells grown on coverslips were fixed in 45% (vol/vol) acetone/10% (wt / vol) formaldehyde/0.1 M phosphate buffer for 5 min. After being washed six times with phosphate-buffered saline, cells were blocked with 1% non-fat milk/1.5% goat serum or horse serum in phosphate buffer for 4 hours at room temperature. The RB-WL-1 anti-RB antibody or Canji's monoclonal anti-RB antibody (QED, San Diego, CA) was diluted to 2 μg/ml or 0.5 μg/ml respectively in the same solution plus 0.02% Triton X-100, and was incubated with the cell overnight. After being washed, the coverslips were processed for immunostaining with the avidin biotinylated peroxidase complex (ABC) method according to the technical manual (Vector Laboratories, Burlingame, CA).

E. Immunoblotting for pRB

Cell lysate was prepared as previously described (Xu *et al.*, 1991a; 1991b). Briefly, cultured cells in 60 mm dishes were lysed with 0.6 ml of ice-cold lysis buffer containing 100 mM NaCl, 0.2% NP-40, 0.2% sodium deoxycholate, 0.1% SDS and 50 mM Tris-HCl (pH8.0) with 50 μg/ml aprotinin and 1 mM PMSF. The cell lysate was passed through 21 gauge needle several times and clarified by centrifugation.

Direct Western immunoblotting was done as described previously (Xu *et al.*, 1991a; 1991b). Sixty micrograms of total cellular protein as determined by the Bradford protein assay (BioRad, Richmond, CA) was electrophoresed in an 8% SDS/polyacrylamide gel and electroblotted to Immobilon polyvinylidene difluoride membranes (PVDF) (Millipore, Bedford, MA). After being blocked with 4% bovine serum albumin/1% normal goat serum in Tris-buffered saline, membranes were incubated overnight with RB-WL-1 antibody at a final concentration of 0.4 μg/ml for RB detection. The blots were then probed by the ProtoBlot Western blot alkaline phosphatase system (Promega, Madison, WI).

F. Growth Curve Measurement

A crystal violet staining method was used to measure the cell growth changes in the presence or absence of tetracycline (Gillies *et al.*, 1986). Briefly, cells were seeded into 24-well plates in duplicate. In one set of the plates, cells were grown in medium containing 0.5 μg/ml

tetracycline, while in duplicate plates, the same cells were cultured in non-tetracycline media. At each time point, cells were fixed with 1% glutaraldehyde in PBS and stained using 0.5% of crystal violet. After cells at all desired time points were collected, the crystal violet dye was extracted from the stained cells by incubating cells with Sorenson's solution containing 0.9% trisodium citrate, 0.02 N chloric acid and 45% ethanol (vol/vol). The extracted dyes were diluted properly with the Sorenson's solution and optical absorbencies at λ_{550} were measured. Growth curves were obtained by plotting the OD_{550} against the time.

G. Soft Agar Assay

For soft agar assay, appropriate number of cells were mixed with 0.3% of agarose in complete medium containing 15% FBS and overlaid onto 0.7% base agar in a 35 mm tissue culture dish. Duplicate dishes were prepared for each individual cell clones. Cells in one dish were cultured in the medium containing 0.5 μg/ml of tetracycline and the other cultured in non-tetracycline medium. The medium was replenished every 3 days, and colonies (>50 cells) were counted after 3 weeks. Results were calculated as the average of three dishes per cell clone.

H. Tumorigenicity Test in Nude Mice

The tumorigenicity test has been described previously (Takahashi *et al.*, 1991). Two groups of athymus nude mice were set up for each cell clone to be tested. One group of mice were given regular water, while the other group was given water containing 5 mg/ml of tetracycline. A total of 5×10^6 cells from each RB^{110}- or RB^{94}-reconstituted clone were injected subcutaneously in 0.2 ml of phosphate buffered saline into the right flank of nude mice. RB-negative parental controls including Saos2, 5637 and MDA-468 cells were injected at the identical concentration into the left flank of the same mice. Tumors were scored 4 weeks after injection.

I. Time Course Study of [^{3}H]-Thymidine Incorporation

Cells from inducible RB-reconstituted clones were grown on sterile coverslips in medium containing tetracycline. At specified time point after removal of tetracycline from the culture medium, the cells were incubated with 1 ml of fresh medium containing 10 μCi [^{3}H]-methyl thymidine (Amersham, Arlington Heights, IL) for 2 hours at 37°C, then fixed and immunochemically stained for expression of RB protein as described previously (Xu *et al.*,

1991a; 1991b). Stained slides were subsequently coated with a thin layer of gelatin and dried at 37°C overnight. The slides were then overlaid with autoradiographic emulsion (Type NTB2, Eastman Kodak, Rochester, NY) and exposed for 2 days. After development, slides were examined under a light microscope.

5

J. [^{3}H]-Thymidine Incorporation of Transiently Transfected Cell Cultures

Tumor cells were seeded onto coverslips and transfected with plasmids expressing pRB^{94}, pRB^{110} or other mutant RB proteins. Twenty-four hours after transfection, cells were processed for immunocytochemical staining of RB protein and [^{3}H]-thymidine incorporation assay as 10 described in Xu *et al.*, 1994a; 1994b.

K. Characterization of Long-Term Inducible RB Expression Clones

The cell growth suppression and morphological changes after RB replacement that have been reported in the literature are inconsistent. Studies done by the inventors and others 15 indicated that replacement of the normal *RB* gene into *RB*-defective tumor cells could suppress their tumorigenic activity in nude mice (Goodrich and Lee 1993, Bookstein *al et.* 1990a; 1990b; Chen *et al.*, 1992; Goodrich *et al.*, 1992; Huang *et al.*, 1988 ; Kratzke *et al.*, 1993; Madreperla *et al.*, 1991; Muncaster *et al.*, 1992; Ookawa *et al.*, 1993; Sumegi *et al.*, 1990; Takahashi *et al.*, 1991; Wang *et al.*, 1993; Xu *et al.*, 1996a; Xu *et al.*, 1991c; Zhou *et al.*, 1994b; Xu 1995; Li 20 *et al.*, 1996; Xu *et al.*, 1994b). The tumor cell lines studied were derived from widely disparate types of human cancers such as the retinoblastoma, osteosarcoma, carcinomas of the bladder, prostate, breast and lung (Goodrich and Lee, 1993; Xu, 1996b; Xu, 1995 for review). Although it has been well documented that correction of the *RB* gene defect alone in tumor cells carrying multiple genetic alterations was sufficient to revert their malignant phenotype, it was more 25 puzzling than it appeared at first sight (Klein, 1990).

As was shown in several early studies, after transient transfection with pRB-expressing plasmids, some types of the *RB*-defective tumor cells in culture displayed striking changes, including cell enlargement, senescent-like phenotype and growth cessation (Templeton *et al.*, 30 1991; Qin *et al.*, 1992). Subsequently, it was found that, however, long-term stable clones of the *RB*-reconstituted tumor cells can be isolated that grew just as rapidly as the parental lines. Therefore, there has been a tendency in the literature to separate the inhibition of cell growth by

RB replacement in *RB*-defective tumor cells from its tumor suppression function (Chen *et al.*, 1992; Goodrich *et al.*, 1992; Takahashi *et al.*, 1991; Xu *et al.*, 1991b; Zhou *et al.*, 1994b; Li *et al.*, 1996).

Three RB-defective tumor cell lines were used to establish long-term inducible RB expression clones. They were the osteosarcoma cell line, Saos2, the bladder cancer cell line, 5637 and the breast cancer cell line, MDA-468. The rationale for choosing Saos2, 5637 and MDA-468 as recipient cells was that they are the RB-defective tumor cells most in use for RB-replacement studies. The tumor cells were transfected with the inducible RB^{110} expression plasmid, pCMV*-tTA-RB^{110} and the pRB^{94} expression plasmid, pCMV*-tTA-RB^{94} in the presence of tetracycline. After selection in 400 μg/ml of G418 for approximately 2 to 4 weeks, well separated single colonies were isolated and maintained in tetracycline containing media. A small portion of the isolated clones were cultured separately in the absence of tetracycline (Tc) for 24 to 48 hours and stained with an anti-RB antibody, RB-WL-1. Tight control of pRB protein expression in the stable clones of Tc-responsive *RB*-reconstituted 5637 bladder carcinoma and MDA-MB-468 breast carcinoma cells is seen.

The RB-reconstituted 5637 cells grown in the presence of 0.5 μg/ml of Tc in the culture medium are RB^- by immunocytochemical staining, while after removal of Tc, the pRB expression was turned on in the RB-reconstituted 5637 cells as shown by RB^+ immunocytochemical staining. The MDA-MB-468 breast carcinoma tumor cells were also RB^- by immunocytochemical staining in the presence of 0.5 μg/ml of Tc in culture medium, whereas after removal of Tc, the pRB expression was turned on in the RB-reconstituted MDA-MB-468 breast carcinoma cells as shown by RB^+ immunocytochemical staining. Note that tetracycline is an inhibitor, rather than an inducer, in this tetracycline-responsive expression system.

The minimal concentration of tetracycline required to shut off RB expression was also tested. It was found that as little as 0.1 μg/ml of tetracycline can inhibit RB expression to non-detectable level by immunostaining, indicating that the tetracycline-regulated expression system is very sensitive to tetracycline.

Additionally, it was surprisingly found that, unlike the non-regulatable, long-term *RB*-reconstituted tumor cell lines previously reported, all the long-term tumor cell clones examined irreversibly ceased growing after pRB expression was turned on in Tc-free medium (FIG. 3A, FIG. 3B and FIG. 3C). It is known in the literature that the half-life of pRB in normal and tumor cells is only 4 to 6 hours (Mihara *et al.*, 1989; Xu *et al.*, 1994b; Xu *et al.*, 1989a), and as was illustrated in FIG. 2, using the modified tetracycline-regulatable system, expression of tTA transactivator *per se* in the presence or absence of low concentration of Tc had no effect on cell growth.

The cell lines also failed to synthesize DNA, which were followed by noticeable morphological changes and finally, by cell death. In the case of the bladder carcinoma cell line, 5637, changes in morphology and growth rate after either transient or stable RB-replacement with a non-regulatable system have not been well documented in the literature (Goodrich *et al.*, 1992; Takahashi *et al.*, 1991; Zhou *et al.*, 1994b).

In general, the phenotypes of the established Tc-regulatable RB^+ tumor lines in Tc-free medium were quite similar to those documented previously for RB plasmid-transfected (or RB retrovirus vector-infected) tumor cell mass cultures (Huang *et al.*, 1988; Templeton *et al.*, 1991; Qin *et al.*, 1992). All tumor cell clones under permissive condition for pRB expression were unable to form colonies in soft agar (FIG. 4A, FIG. 4B and FIG. 4C), and were non-tumorigenic in nude mice.

To compare *RB* with another common tumor suppressor gene, *p53*, several long-term stable tumor cell clones with Tc-regulatable wild-type p53 expression have been established from the osteosarcoma cell line, Saos-2. A similar approach as described above was used to establish the p53-reconstituted Saos-2 tumor cell clones. In brief, the parental Saos-2 tumor cells were transfected with the wild-type p53-expressing plasmid, pCMV*-tTA-p53 (Example 4) and selected in geneticin-containing media. The initial G418-resistant mass cultures were subjected to at least two rounds of subcloning in order to obtain stable wild-type *p53*-reconstituted clones. Because of complete deletion of the *p53* gene, the parental Saos-2 cells have no endogenous p53.

With this model system, it was found that induction of wild-type p53 expression in *p53*-reconstituted Saos-2 clones did result in growth arrest of the $RB^-/p53^{null}$ tumor cells. When the Tc-regulated *p53*-reconstituted Saos-2 clones were grown in the absence of Tc, many tumor cells shrank and detached. Furthermore, as measured by DNA fragmentation assay, abundant low molecular weight DNAs were detected only in samples extracted from *p53*-reconstituted Saos-2 tumor cells under permissive condition for p53 expression. These observations indicate that the wild-type p53-induced growth arrest of the $RB^-/p53^{null}$ Saos-2 tumor cells was the result of apoptotic cell death rather than replicative senescence.

Dimri *et al.*, recently reported a biomarker that identifies senescent human cells in culture and in aging skin *in vivo*. It was show that several human senescent cells expressed a β-galactosidase, histochemically detectable at pH 6 (Dimri *et al.*, 1995). This marker, termed senescence-associated β-galactosidase (SA-β-gal), is expressed by senescent, but not pre-senescent fibroblasts. SA-β-gal was also absent from immortal cells, but was induced by genetic manipulations that reversed immortality (Dimri *et al.*, 1995). Of note, some cells, such as adult melanocytes, expressed the SA-β-gal (pH 6 activity) independent of senescence or age. Thus, SA-β-gal is not a universal marker of replicative senescence, which is not surprising.

Nevertheless, by utilizing the instant long-term tumor cell clones with tetracycline-regulatable pRB or p53 expression, the SA-β-gal (pH 6 activity) provides a simple assay allowing the further characterization the RB-mediated tumor cell growth cessation. The majority (>99.9%) of young (early passage) human WI-38 fibroblasts are SA-β-gal negative. In contrast, the senescent (at population doubling level greater than 52) WI-38 cells were strongly SA-β-gal positive. All tetracycline-responsive tumor cell clones examined so far were SA-β-gal negative in the presence of tetracycline (RB^-), and were SA-β-gal positive in tetracycline-free medium (RB^+). The intensity of SA-β-gal staining of tumor cells in RB^+ status, however, was variable depending on tumor cell types.

Of note, although p53 reconstitution in Saos-2 (RB^-, $p53^{null}$) tumor cells with either non-inducible (Chen *et al.*, 1990; Li *et al.*, 1996) or inducible system did suppress their neoplastic phenotype, the p53 reconstituted Saos-2 clones with the tetracycline-regulatable promoter were

SA-β-gal negative in either presence or absence of tetracycline. Of great interest, when the p53-reconstituted Saos-2 cells were infected with recombinant adenovirus vectors expressing the wild-type pRB^{110} in Tc-free medium, the tumor cells with both wild-type p53 and pRB^{110} expression displayed more intense SA-β-gal positive staining as compared to tumor cells only expressing pRB^{110}. The results imply that the mechanisms for tumor suppression by pRB and p53 were different from each other, but expression of pRB and p53 together had synergistic effects on RB-mediated tumor cell senescence.

In consideration of its potential therapeutic use, another important finding was the fact that the pRB-mediated replicative senescence (irreversible growth cessation) was tumor-specific. The young WI-38 fibroblasts at early passage infected with recombinant adenovirus vector, AdCMVpRB110 at multiplicity of infection (MOI) of 100 remained SA-β-gal negative, and they resumed a normal growth pattern about one week post-infection. Therefore pRB is a relatively safe reagents for anticancer gene therapy. In addition to therapy of advanced malignancies, the emerging RB gene therapy also may be beneficial in treating post-surgery residue tumors, superficial cancers, or premalignancies, as well as non-malignant, hyperproliferative disorders in certain circumstances (Chang *et al.*, 1995; Xu *et al.*, 1996a).

L. The broad biological basis of the *RB*-mediated tumor suppression.

In addition to tumor cell-specific senescence and the well-known antiproliferative effects, pRB may also play a role in inhibition of angiogenesis and in elicitation of immunogenicity of tumor cells. The inventors have shown that serum-free conditioned media (CM) collected from the tetracycline-responsive, *RB*-reconstituted osteosarcoma and non-small cell lung carcinoma cell lines switched from angiogenic to anti-angiogenic after removal of Tc from the cell cultures. This switch corresponded with the onset of pRB expression as determined by Western blotting and immunohistochemistry (Dawson *et al.*, 1996). The inventors have also reported that HLA class II induction by IFN-γ in the RB-defective non-small cell lung carcinoma cell line, H2009, requires reconstitution of the wild-type RB gene expression (Lu *et al.*, 1996). The class II proteins present peptides derived from proteolytically processed antigens to $CD4^+$ T lymphocytes as part of the immune response. Therefore, pRB likely has a role in mediating tumor immunogenicity as well.

To determine if replacement of the retinoblastoma (*RB*) tumor suppressor gene could inhibit invasion of *RB*-defective tumor cells, studies were conducted using the Boyden chamber assay (Li *et al.*, 1996). The studies were done in a diverse group of stable *RB*-reconstituted human tumor cell lines, including those derived from the osteosarcoma and carcinomas of the bladder, breast and lung. The expression of the exogenous wild-type RB protein in these tumor cell lines was driven by either a constitutively active promoter or an inducible promoter. It was found that significantly more tumor cells from the parental *RB*-defective cell lines and the RB revertants than from the *RB*-reconstituted RB^+ cell lines penetrated through the Matrigel in the Boyden chamber assay ($p < 0.001$, two-tailed t-test). Of note, the inhibition of invasiveness of various *RB*-defective tumor cells by *RB* replacement was apparently well correlated with suppression of their tumorigenicity *in vivo*. In contrast, although either functional *RB* or p53 re-expression effectively suppressed tumor formation in nude mice of the $RB^-/p53^{null}$ osteosarcoma cell line, Saos-2, replacement of the wild-type p53 gene had much less impact on their invasiveness as compared to the *RB* gene.

Normal human diploid cells senesce *in vitro* and *in vivo* after a limited number of cell divisions. This process known as cellular senescence is an underlying cause of aging and a critical barrier for development of human cancers. It has also been demonstrated that *RB/p53*-defective tumor cells reexpressing functional pRB alone *via* a modified tetracycline-regulated gene expression system were irreversibly growth-arrested at G0/G1 phase of the cell cycle. These cells displayed multiple morphological changes consistent with cellular senescence and also expressed a senescence-associated β-galactosidase biomarker.

Further studies indicated that telomerase activity, which was presumably essential for an extended proliferative life-span of neoplastic cells, was repressed in the tumor cell lines after induction of pRB (but not p53) expression. These observations suggest that pRB plays a critical role in the intrinsic cellular senescence program. From a practical standpoint, findings imply that cytostatic gene therapy using *RB* (or *RB* and *p53* together) may result in differential elimination of tumor cells through cellular senescence and crisis. At the same time the replicative lifespan of

normal cells *in vivo* may not be affected. This could provide a potential basis for designing tumor-specific tumor suppressor gene therapy and anti-telomerase gene therapy.

These findings, taken together, may intimate that the *RB*-mediated tumor suppression has a broad biological basis, which certainly makes the emerging *RB* tumor suppressor gene therapy for human cancer even more attractive.

M. Enhanced Tumor Suppression by an N-terminal Truncated pRB.

Long-term stable clones of the *RB*-reconstituted tumor cells can be isolated with non-inducible gene expression systems, and most of these clones grow just as rapidly as the parental lines. The inventors have also found that, although the *RB*-mediated tumor suppression was substantial and had a broad biological basis, it was often incomplete and a portion of the *RB*-reconstituted tumor cells were able to survive and form RB^+ xenograft tumors in nude mice after a prolonged latency period (Takahashi *et al.*, 1991; Xu *et al.*, 1991b; Zhou *et al.*, 1994b; Li *et al.*, 1996). Similar observations have been reported by other investigators (Bookstein *et al.*, 1990b; Goodrich *et al.*, 1992; Kratzke *et al.*, 1993; Ookawa *et al.*, 1993; Wang *et al.*, 1993). This phenomenon is referred to by the inventors as *tumor suppressor resistance* (TSR; Zhou *et al.*, 1994b), which is an equivalent of multiple drug resistance (MDR) in chemotherapeutics. In the latter scenario, low-dose chemotherapy may risk the selection of metastatic tumor cells due to their often inherently higher resistance to cytotoxic agents.

The inventors subsequently reported that an N-terminal truncated RB protein of ~94 kDa (pRB^{94}) exerted surprisingly more potent cell growth suppression as compared to the full-length pRB protein in a diversity of tumor cell lines examined, including those having a normal endogenous RB gene. Tumor cells transfected with the pRB^{94}-expressing plasmids displayed multiple morphological changes frequently associated with cellular senescence. They failed to enter S phase and rapidly died (Xu *et al.*, 1994b; Resnitzky and Reed, 1995).

The inventors recent studies in ectopic animal models demonstrated that treatment of established human RB^- and RB^+ bladder xenograft cancers in nude mice by AdCMVpRB94, a replication-deficient adenovirus vector expressing the N-terminal truncated RB protein, resulted in regression of the treated tumors (Xu *et al.*, 1996a). Of note, although both the full-length and

the truncated forms of the RB protein, when over-expressed in tumor cells via adenovirus vectors, were capable of suppression of tumor growth, the pRB^{94} was much more potent than the full-length RB protein. The mechanism for the enhanced tumor suppression by the N-terminal truncated RB protein is not clear yet.

To better understand the functional difference between the N-terminal truncated pRB^{94} and the full-length pRB^{110}, the inventors have also established stable tumor cell lines with Tc-responsive pRB^{94} expression. By time course analysis, it was found that as early as 6 hours after removal of tetracycline from the cell culture medium, the pRB^{94}-reconstituted tumor cells accumulated the maximum of both underphosphorylated and phosphorylated pRB^{94}, followed by failure of the vast majority of the tumor cells to incorporate ^{3}H-thymidine, an indicator of growth cessation. The pRB^{94} protein was completely dephosphorylated within ~18 to 24 hours. Most of the pRB^{110}-reconstituted tumor cells, however, remained immunohistochemically RB^- at the 6 or 8 hr-time points and had normal DNA synthesis (FIG. 5). The pRB^{110} reached the highest level at the 24 hr-time point as determined by western blotting, and became mostly unphosphorylated from 24 to 48 hours after removal of tetracycline, in which period the pRB^{110}-reconstituted tumor cells finally ceased DNA synthesis (FIG. 5). Using the SA-β-gal biomarker assay for human senescent cells, it was shown that the Saos-2 cells with pRB^{94} expression showed more intense SA-β-gal positive staining as compared to the pRB^{110}-expressing cells at 48 hr after removal of Tc. Since pRB^{94} has a longer half-life than pRB^{110} and tends to remain in an active, underphosphorylated form (U. S. Patent No. 5,496,731; Xu *et al.*, 1994b), rapid accumulation of mostly the active forms (underphosphorylated form) of RB protein in the tumor cells may account for the enhanced tumor cell growth suppression by pRB^{94}. In this regard, another truncated version of pRB, named pRB^{56}, beginning at amino acid 379, has also been reported as a more potent inhibitor of cell cycle progression compared to the full-length pRB (Wills *et al.*, 1995).

The advantages of the modified system are threefold: 1) it is suitable for establishing long-term stable cell lines with inducible gene expression because of lower constitutive

expression of the tTA peptide; 2) the system is now contained within a single plasmid so that only one round of transfection and selection is required; and 3) of importance, the single-plasmid tetracycline-responsive mammalian gene expression system is readily convertible to tetracycline-controlled viral vectors (Examples 6-11 below).

EXAMPLE 6

Construction of Tetracycline-Controlled Adenoviral Vectors

The desired cDNA fragment of a gene of interest is first inserted into the single-plasmid tetracycline-regulatable plasmid vector, EC1214A (Example 2) or EC1214B (Example 3). The tetracycline-responsive foreign gene expression cassette and the modified tTA (or rtTA) expression cassette from the corresponding EC1214A or EC1214B plasmid vectors are then recovered using standard methods in the art for DNA manipulation (Maniatis *et al.*, 1989; Ausubel *et al.*, 1992), and inserted into the shuttle plasmid, pΔE1sp1A (Microbix Biosystems, Inc.). The resultant recombinant shuttle plasmids are then co-transfected with the master adenovirus type 5 (Ad5) plasmid, pBHG11, which contains the backbone of the adenovirus Ad5dl309 genome and E1/E3 deletion mutation (Microbix Biosystems, Inc.) into 293 cells using the LIPOFECTIN reagent (GIBCO/BRL Life Technologies). The co-transfection of 293 cells is performed in the presence (for tet-off system) or absence (for tet-on system) of 0.5 μg/ml of tetracycline.

Alternatively, a fragment containing a gene of interest is first inserted into the single-plasmid tetracycline-regulatable plasmid vector, EC1214A or EC1214B. The tetracycline-responsive foreign gene expression cassette and the modified tTA (or rtTA) expression cassette from the corresponding EC1214A or EC1214B plasmid vectors are then recovered and inserted, respectively, into the shuttle plasmid, pΔE1sp1A and the master adenovirus plasmid, pBHG11. The resultant recombinant shuttle plasmids and the recombinant master adenovirus plasmid are co-transfected into 293 cells.

Co-transfection of 293 cells with the recombinant shuttle plasmid and the recombinant master adenovirus plasmid produce infectious virions by *in vivo* recombination, in which the minigene cassette expressing the gene of interest and the modified tTA (or rtTA) expression

cassette are replaced the ΔE1 region or ΔE1 and ΔE3 regions of the Ad5dl309 genome, respectively. Presence of recombinant adenoviruses in the transfected 293 cells is initially identified by cytopathic effect (CPE). Cell culture supernatants are collected from the transfected 293 cells in which CPE has occurred. Recombinant viruses are then isolated by screening adenovirus plaques from 293 cell monolayers after infection with the virus supernatants, and further characterized by restriction enzyme digestion mapping, PCR™, or by expression of the gene of interest in virus-infected host cells in a tetracycline-regulatable manner. The recombinant adenoviruses containing the desired foreign gene as well as the modified tTA (or rtTA) expression cassettes are subjected to at least three rounds of plaque purification.

High-titer stocks of the tetracycline-controlled recombinant adenoviruses are prepared by methods modified from Graham, and Prevec, (1991). The CsCl ultracentrifugation-purified adenoviruses contain ~10^{13} viral particles per ml as measured by OD at 260 nm (1 OD_{260} = 1 × 10^{12} viral particles per ml). The concentrated viral suspension is desalted by gel filtration through Sephadex G50 to generate a final purified virus stock about 10^{11} plaque-forming units (pfu) per ml in PBS.

EXAMPLE 7

Preparation of Tetracycline-Responsive TNFα Adenovirus Vector

Tumor Necrosis Factor (TNFα; Pennica, *et al.*, 1984) has been used in clinical protocols to treat metastatic prostate cancer, but the efficacy of the conventional TNFα chemotherapy is limited by its systemic toxicity (Brouckaert, *et al.*, 1992). The inventors reasoned, therefore, that local administration of high-dose TNFα directly into the metastatic sites of the prostate cancer (often in bone marrow) should more effectively kill the tumor cells, while reducing the systemic toxicity of TNFα.

The modified single-plasmid tetracycline-regulatable gene expression system as described in Example 2 is readily convertible to tetracycline-controlled viral vectors. The single-plasmid vector with a CAT reporter gene inserted into the *Hin*dIII/*Bam*HI cloning site expressed only moderate CAT activity in 293 cells (Example 1), even though the 293 cells contain the E1a

protein, which is known to be a potential transactivator of the conventional CMV promoter (Gorman *et al.*, 1989).

The modified tetracycline-responsive mammalian gene expression system with no squelching effects on host cell growth has been used to generate a recombinant adenovirus vector with E1/E3 deletion mutation, named AdVtTA.TNFα. The modified tTA expression cassette and the tetracycline-responsive TNFα expression cassette are inserted, respectively, into a master plasmid, pBHG11 (Microbix Biosystems, Inc.), which contains the Ad5 E1/E3 deletion mutant genome, and into a shuttle plasmid, pΔE1sp1A. The resultant plasmids, pBHG.tTA and pΔE1.TNFα are then co-transfected into 293 cells (ATCC CRL1573) to produce infectious virions by *in vivo* recombination. In an alternate method of constructing AdVtTA.TNFα the entire tetracycline regulation cassette is inserted into the E1 region of the adenovirus genome.

This novel adenovirus, AdVtTA.TNFα, was characterized by restriction enzyme digestion mapping and by standard human TNFα ELISA assay. The leakage expression of hTNFα by AdVtTA.TNFα was very low when the cell culture medium contained as low as 0.1 μg/ml tetracycline, whereas it produced high titer of TNFα in host cells under permissive condition (in Tc-free medium). The low base-line expression of TNFα by AdVtTA.TNFα was quite impressive in the replication-competent 293 cells, even after the cytopathic effect had been complete following the adenovirus propagation.

The cell lines tested involved various human tumor types, human and murine T lymphocytes. The hTNFα production by AdVtTA.TNFα-transduced human mature T cell line, HUT 78, was at the levels of ~5,000 to 10,000 pg/ml/10^6 cells/24hr, which were significantly higher than retroviral vector-mediated hTNFα production as was documented in the literature (Hwu and Rosenberg, 1994). The HUT 78 has properties of mature T cells with inducer/helper phenotype and releases IL-2 (ATCC TIB-161). The non-transduced HUT 78 cells produced undetectable levels of hTNFα, and even at the highest multiplicity of infection examined (MOI= 200), the production of hTNFα by AdVtTA.TNFα-transduced HUT 78 was readily turned off in medium containing 0.1 μg/ml of Tc (FIG. 6). The transduced HUT 78 cells persistently secreted high concentration of hTNFα in Tc-free medium at one week post-AdVtTA.TNFα infection.

The hTNFα secreted by AdVtTA.TNFα-transduced human T cells was biologically active as determined using the standard L929 cytolytic assay (FIG. 7). Moreover, the AdVtTA.TNFα-infected mouse cytotoxic T cell line, CTLL-2, also secreted comparably high levels of hTNFα in a tetracycline-regulatable manner. CTLL-2 is an IL-2-dependent T cell line obtained from ATCC (TIB-214). In this connection, it has previously been reported by others that non-regulatable recombinant adenoviral vectors derived from human adenovirus type 5 were able to more efficiently (as compared to retroviral vectors) transduce murine $CD8^+$ tumor-infiltrating lymphocytes (TIL) and the resultant gene-modified TIL secreted high concentration of interleukin-2 or interleukin-7 (Nakamura *et al.*, 1994).

The leakage expression of TNFα by AdVtTA.TNFα in the replication-competent 293 cells following propagation of the adenovirus vector was also impressively low. This provides the rationale that the approach will have broad utilities ranging from cytokine gene to tumor suppressor gene therapy. For instance, this system may facilitate generating various recombinant adenovirus vectors with insertional gene expression that are potentially highly cytotoxic or cytostatic to the adenovirus producer cells. It may also be a useful approach for improving the quantity and quality (*e.g.*, the ratio of plaque-forming units to viral particles) of the virus supernatant in many circumstances.

The results above confirm this approach, since the yield of AdVtTA.TNFα was increased about 10-fold when it was propagated in 293 producer cells under non-permissive versus permissive conditions. In fact, the inventors initial attempts to generate TNFα adenovirus vectors using a non-inducible promoter were unsuccessful, probably because the adenovirus E1a protein normally expressed in the 293 cells sensitizes the cells to the cytotoxic effects of TNFα (Shisler *et al.*, 1996).

A. Bone-specific Delivery of TNF by Gene-modified Bone Marrow (BM) Cells

The replication-deficient, tetracycline-responsive adenovirus may be used for organ-specific administration of TNFα via bone marrow (BM) mononuclear cells, which would result in a novel treatment for metastatic prostate cancer. The treatment involves *ex vivo* infection of BM mononuclear cells with AdVtTA.TNFα under non-permissive conditions and administration of the infected autologous mononuclear cells in the general circulation of patients.

Since the bone marrow is the natural home organ of the BM cells, the *ex vivo* transduced BM cells will accumulate and incorporate into patients' bone marrow after administration, where the metastatic prostate cancer cells frequently harbor. It is hoped that the genetically modified BM cells will express high-level TNFα and efficiently kill the adjacent cancer cells in the bone marrow.

It is possible that the transduced BM cells may overproduce TNFα after being administered to a patient in the general circulation. In this regard, one of the major advantages of this vector system is that the expression of TNFα from the AdVtTA.TNFα adenovirus vector is controllable by a low-dose tetracycline. Accordingly, to minimize the systemic toxicity of TNFα, tetracycline may be administered to treated patients during the period when the majority of the TNFα-transduced BM cells in the circulation are still on their way to the bone marrow.

Finally, this system, which uses adenoviral vectors rather than retroviral vectors, is particularly suitable for TNFα (or other cytokine) gene transfer in treatment of cancer, because this type of cancer gene therapy does not require sustained gene expression. The BM cells will express TNFα at high levels immediately after transduction by the recombinant adenovirus vector, but the TNFα activity will decrease gradually with passage due to the fact that the viral genome is diluted out by cell division (integration of adenovirus into the host genome is very rare in human cells). Therefore, this novel system for gene therapy of metastatic prostate cancer will be relatively safe.

The other advantages of the tetracycline-controlled adenovirus vectors include potential higher virus titers/yields, and high quality of the virus supernatants (lower ratio of viral particles to plaque-forming units). Therefore, the system will have broad utilities ranging from cytokine gene and tumor suppressor gene therapy, to tumor vaccines (immunotherapy).

B. Bone-specific delivery of TNF through gene-modified osteoblast

A novel adenovirus vector, AdVtTA.OG.TNF-α, was constructed to conduct osteoblast-specific (bone-specific), autoregulatable and tetracycline-regulatable TNFα gene expression. AdVtTa.OG.TNFα is used for bone-specific delivery of high-dose TNFα gene therapy for prostate cancer, metastatic to bone. The plasmid pII1.3luc, containing the promoter from the

best-characterized osteoblast-specific mouse osteocalcin gene 2 (mOG2; Ducy and Karsenty, 1995), was used to obtain the mOG2 promoter. In transgenic mice, 1.3 kb of the promoter of the human osteocalcin gene is active only in osteoblasts (Kesterson, 1993). A region located between -147 and -34 contains all of the regulatory elements required for osteoblast-specific expression (Ducy and Karsenty ,1995).

An ~700 bp fragment of the mOG2 promoter, named TNF.OGp, was derived from plasmid pII1.3luc by inserting a TNF α-responsive motif contained within a *Bgl*II/*Xho*II adaptor (5'-AAGATCTAGGCTGCCTGGATCCT-3'; top strand (SEQ ID NO:5) and 5'-AGGATCCAGGCAGCCTAGATCTT-3'; bottom strand (SEQ ID NO:6); motif underlined; Li and Stashenko, 1993) at -327 and by PCR™ amplification of the mOG2 promoter sequence from -657 to +13 using oligo II (SEQ ID NO:30; 5'-CTCGAGCCAAGACCTGGCCCAG-3') and oligo III (SEQ ID NO:31; 5'-ATCTAGATGGTCGACTTGTCTGT-3') as primers. When the TNF.OGp promoter replaced the mCMVp in EC1214A, it expressed intermediate CAT gene activity, comparable to mCMVp, in osteoblastic cell lines, but in no other cell line. The CAT expression was significantly down-regulated by presence of TNFα in the medium. TNFα production from the recombinant adenoviral genome is 1) bone-specific; 2) controlled by Tc; and 3) down-regulated by TNFα itself through down-regulating the tTA transactivator (TetR.VP16). The autoregulation provides the osteoblast cell and the host with additional protection from augmentation of systemic toxicity due to overexpressing TNFα.

Several skeletal metastasis models of human prostate cancer have been reported (Shevrin *et al.*, 1988; Wang and Stearns, 1991; Thalmann *et al.*, 1994). Recently, a new osseous metastasis model, which uses direct injection of androgen-independent PC-3 cells into the femur medullas of Beige nude mice was reported. The intra-femorally injected cells formed tumors in the bone of 100% the recipients and metastasized to local lymph nodes (Soos *et al.*, 1996). This model will be used for systemic TNFα gene therapy. The Tc-regulatable TNFα viral vector transduced BM cells, or the bone-specific AdVtTA.OG.TNF-α vector will be administered to tumor-bearing mice through the tail vein. The treatments can be repeated as needed. The TNFα levels in the peripheral blood will be monitored daily by ELISA assay. Different therapy regimens will be tested in the animal model, including combination TNFα gene therapy and chemotherapy. The expression of TNFα can be adjusted by changing the doxycycline supply in

drinking water. Since metastatic prostate cancer is often associated with osteoblastic rather than osteolytical lesions (Achbarou *et al.*, 1994), this may provide a unique opportunity for the osteoblast-specific adenoviral vector.

C. ***in vivo* Cytokine Gene Therapy of Prostate Cancer Using the Beige Nude Mouse Bone Metastatic Model**

Male Beige nude mice (deficient in T and NK cells) and prostate carcinoma cell line PC-3 (available from ATCC) will be tested with: 1) replication-deficient (E1/E3 deletion) recombinant adenovirus AdVtTA.TNFα, expressing human TNFα in tetracycline-regulatable manner; 2) AdVtTA.Os.TNFα, expressing human TNFα in osteoblasts in a tetracycline-regulatable manner; 3) AdCMVpβ-gal, expressing β-galactosidase (control); and 4) safety-modified retroviral vectors, expressing human TNFα in a tetracycline-regulatable manner.

30 mice, 10 mice per group will be used. The mice will be anesthetized with 60 mg/kg of ketamine *i.p.* (or by metofane inhalation to effect) under sterile conditions. The level of anesthesia will be monitored and adjusted based on heart rate, respiratory rate and muscle activity of the animal. Then a 3-mm incision will be made over the patella of the right-hind limb. The patella will be retracted laterally. A 26-gauge needle will be used to perforate the condylar surface of the distal femur of the right-hind leg, to cannulate the inner femoral marrow cavity. Then 1×10^6 of PC-3 tumor cells in 30 µl of PBS will be injected into the marrow cavity of the right femur. Following injection, hemostasis will be achieved with direct pressure and the wound will be closed with a single clip. Each mouse will be monitored to ensure uneventful recovery from anesthesia and a warming blanket will be used during the recovery period.

Following surgery, no significant physiological disturbance from the experimental procedure performed is expected. The wound will be examined at ~24 hours after the procedure for evidence of infection. Any mouse demonstrating evidence of infection or impairment with normal ambulation will be euthanized immediately.

The intra-femorally injected PC-3 cells should form prostate tumors in the bone of 100% of the recipients, invade into the surrounding muscle tissue and subsequently metastasize to local lymph nodes (Soos *et al.*, 1996). Therefore, the potential morbidity that may develop following

this experimental procedure would be femoral shaft destruction as a consequence of tumor invasion and erosion. The animal will be observed daily including weekends for evidence of ambulatory impairment. Any animals which demonstrate ambulatory impairment, or have a palpable mass overlying the area of the right femoral shaft will be euthanized immediately and a necropsy performed.

Two weeks after intra-femoral injection of tumor cells, 1 μg/ml of tetracycline (or doxycycline) will be added to the drinking water for the mice, and the mice will be randomly divided into 3 groups and treated with different therapy regimens: Group A, No treatment (control group); Group B, 10^8-10^9 pfu of AdCMVpβ-gal in 0.1 ml PBS (pH 7.4) or 0.1 ml PBS only will be infused *via* the tail vein (mock viral vector or buffer control); Group C, 10^8-10^9 pfu of AdVtTA.Os.TNFα in 0.1 ml PBS will be administered to animals *via* the tail vein (or AdVtTA.TNFα; or adenoviral/retroviral vector-modified bone marrow cells from syngeneic Beige nude mice).

The tetracycline (or doxycycline) will be removed from the drinking water to allow TNFα expression. The expression of TNFα in the tumor microenvironment by gene-modified bone marrow cells or osteoblasts may be adjusted by changing the tetracycline (or doxycycline) supply in the drinking water. If high-levels of the recombinant hTNFα accumulated in the tumor microenvironment kill the adjacent tumor cells *in vivo*, the bone tumors should shrink and finally disappear (tumor regression). The animals will be observed daily including weekends. The treatment (step 7 and step 8) may be repeated as needed (weekly or biweekly). All mice will be euthanized at week 16 after intra-femoral injection of tumor cells, unless they demonstrate morbidity from the procedure as outlined above, in which case the animal will be euthanized immediately. Following euthanasia, the animals will be brought to radiology for radiographic evaluation of their right femur. Then a necropsy will be performed to evaluate tumor formation in bone, lymph node metastases, and tumor regression after TNFα gene therapy.

EXAMPLE 8

Preparation of Tetracycline-Responsive RB Adenovirus Vector

A replication-deficient adenovirus vectors expressing N-terminal truncated pRB^{94} protein (U. S. Patent No. 5,496,731) has been used in *in vivo* animal studies of human cancer gene therapy (Xu, *et al.*, 1996a). Unfortunately, the ratio of viral particles to plaque-forming units of the AdCMVpRB94 virus supernatants increased dramatically with passage, making it difficult for large-scale preparation of high-titer stocks of the AdCMVpRB94 virus for human cancer gene therapy clinical trials. This was probably caused by the super cell growth suppression effects of pRB94 protein on the 293 virus-producing cell line.

The modified tetracycline-responsive mammalian gene expression system has been used in a similar manner as described above to generate a tetracycline-controlled pRB^{94}-containing adenovirus vector, AdVtTA.RB94. In one method of creating AdVtTA.RB94 the entire tetracycline regulation cassette is inserted into the E1 region of the adenovirus genome. In an alternate method the RB^{94} expression cassette is inserted into the E1 region of the adenovirus genome, while the transcriptional transactivation fusion protein expression cassette is inserted into the E3 region of the adenovirus genome. Over-expression of pRB^{94} in tumor cells will cause tumor cell-specific senescence and cell death. The pRB^{94} cDNA has a modified optimal initiator context sequence. The expression of the pRB94 protein in transduced human tumor cells by AdVtTA.RB94 can be reversibly turned off and on. There is an absence of pRB immunostaining when the 5637 cells are in the presence of 0.5 μg/ml of tetracycline. At the multiplicity of infection used (MOI=200), the leakage expression of pRB94 by AdVtTa.RB94 under non-permissive conditions was undetectable. However, these cells show positive pRB immunostaining in the absence of tetracycline. The pRB protein was detected by a standard immunochemical staining method (Xu *et al.*, 1994b). The novel AdVtTA.RB94 recombinant adenovirus vector can be propagated efficiently in 293 cells with increased yield and quality.

EXAMPLE 9

Preparation of Tetracycline-Responsive RB/p53 Coexpression Vector

As described in Example 5 above, although p53 reconstitution in Saos-2 (RB^-, $p53^{null}$) tumor cells with either non-inducible (Chen *et al.*, 1990; Li *et al.*, 1996) or inducible system did suppress their neoplastic phenotype, the p53 reconstituted Saos-2 clones with the tetracycline-regulatable promoter were SA-β-gal negative in either presence or absence of tetracycline. However, when the p53-reconstituted Saos-2 cells were infected with recombinant adenovirus vectors expressing the wild-type pRB^{110} in Tc-free medium, the tumor cells with both wild-type p53 and pRB^{110} expression displayed more intense SA-β-gal positive staining as compared to tumor cells only expressing pRB^{110}. The results imply that the mechanisms for tumor suppression by pRB and p53 were different from each other, but expression of pRB and p53 together had synergistic effects on RB-mediated tumor cell senescence.

Since co-expression of pRB and p53 has synergistic effects on pRB-mediated, tumor-specific senescence (Example 5), and it has been suggested that altered RB and p53 protein status could be a synergistic prognostic factor in non-small cell lung carcinomas, as well as a subset of other human malignancies, including transitional cell carcinomas of the bladder (Xu, 1995; Xu *et al.*, 1994a; Xu *et al.*, 1996b), combination pRB and p53 gene therapy is also contemplated as an alternative strategy to surmount possible tumor suppressor resistance.

Insertion of both the modified tetracycline-responsive transactivator (tTA) expression cassette and the tTA-dependent pRB^{110} expression cassette into the E1 region of the Ad5 genome facilitates construction of an adenovirus vector simultaneously expressing two tumor suppressor genes, named AdVtTA.RB110/p53. In this vector, the smaller p53 expression cassette is inserted into the E3 region of the 34 kb master plasmid, pBHG11, through ligation reaction. Since attempts to replace both RB and p53 genes in the same cell have never been successful (Wang *et al.*, 1993), the inventors reasoned that adenovirus vectors simultaneously expressing the two tumor suppressor genes should be built in the regulatable gene expression system.

EXAMPLE 10

Construction of Tetracycline-Controlled Retroviral Vectors

1. Novel Human Tumor Cell-Hosted (TCH) cDNA Library

A human cDNA library may contain unknown therapeutic genes for human cancers, such as unknown tumor suppressor genes, programmed cell death (apoptosis) genes, senescence genes, biological clock genes and many other types of cellular regulatory genes. A cDNA library that is built directly in millions of human tumor cells where expression of all the cDNA-encoded genes can be turned on and off reversibly, would allow these therapeutic genes to be identified by random functional selection. The selection is based on measurable phenotypic changes of the host tumor cells after the cDNA gene expression has been turned on.

By using the modified Tc-responsive gene expression system-based retroviral plasmid vector, a novel human cDNA library in retrovirus plasmids with potential Tc-regulatable cDNA gene expression has been constructed. Plasmid DNAs prepared from 100 random colonies were analyzed on a 1% agarose gel. The test result indicated that >90% of the colonies contained recombinant plasmids, and the average insert size was approximately 1.2 kb. The new retroviral plasmid library was converted into retrovirus particles and subsequently into a stable human tumor cell-hosted (TCH) cDNA library.

In this connection, a pseudotype (expressing *gag*, *pol* and vesicular stomatitis virus G protein genes in a Tc-inducible manner) retroviral packaging cell line has recently been established in the 293 cells. Consequently, after transient transfection with plasmid DNAs from the retrovirus plasmid cDNA library, recombinant retroviruses can shuttle back and forth between this pseudotype packaging cell line and an amphotropic packaging cell line (for example, PA317) in a mixed culture ("ping-pong"), leading to boosted virus titers. This greatly facilitates converting the plasmid library into virus particles.

Briefly, the retroviral plasmid library is converted into a mixture of retroviral particles by transfection into 40 dishes (150mm in diameter) containing packaging cells. Approximately 2×10^6 packaging cells are transfected with 20 μg plasmid DNAs *via* LIPOFECTIN in each dish. Twenty-four hours after transfection, the retrovirus-containing tissue culture medium is collected

every 12 hours over 3 days at 32°C. The medium also contains 0.5 μg/ml tetracycline throughout the process. The retrovirus supernatant is purified by filtration through 0.22 μm membranes and immediately used for infection of host human tumor cells.

The purified retrovirus plasmid library-derived retrovirus supernatant is used to infect a long-term tumor clones expressing the modified tTA transactivator cassette, in which tight control of gene expression by tetracycline-responsive promoters has already been verified. For retrovirus infection, the cells are plated in 20 dishes (150mm in diameter) at 2×10^6 cells per dish, and infected with the plasmid library-derived viruses over three days with 12-hours intervals in the presence of 2 μg/ml polybrene and 0.5 μg/ml tetracycline. After the cells recover from the initial viral crisis, the survivors are selected in the media containing G418 (400 μg/ml). A total of 5×10^5 independent G418 resistant clones (approximately 5×10^7 cells) are collected from all 20 dishes. Aliquots of the tumor cell-hosted library are stored in liquid nitrogen.

To evaluate the library, cellular DNAs are prepared from an aliquot of the TCH- library (about 5×10^5 cells) and PCR™ amplification is performed for 40 cycles in a Perkin-Elmer thermal cycler with the synthetic primers designed for rescuing cDNA inserts from the integrated proviruses. Southern blot analysis of the amplified cDNA inserts is carried out using a β-actin hybridization probe. An intense β-actin band of about 2.0-kilobase is detected on the blot.

The final human tumor cell-hosted (TCH) cDNA library consists of 5×10^5 independent single cell clones containing random cDNA inserts derived from human normal fibroblasts. Of importance, in this tumor cell-hosted library, expression of all the human cDNA-encoded genes is under the tight control of a tetracycline-responsive promoter. The TCH-cDNA library described in this example is a prototype of this new class of cDNA libraries. New medical and biological technologies would improve such libraries and make them even more attractive.

2. Alternative Retroviral Vectors

The *kat* retrovirus production system produces high titer retrovirus supernatant capable of transducing efficiently hematopoietic cell types refractory to conventional retrovirus transduction (Finer *et al.*, 1994). The *kat* retrovirus plasmid vector with a hybrid LTR with will be combined with EC1214A (Example 2) to generate a retrovirus with Tc-regulatable TNFα expression.

Since some success using standard retroviral vectors have been reported in the literature, the Tc-controlled retroviral vector may work better than the Tc-controlled adenoviral vector for transduction of hematopoietic stem cells, and will be used, for example, in bone-specific TNFα gene therapy.

EXAMPLE 11

Cytokine Gene-Modified TIL Therapy

This Example provides designs and methods pertinent to regulatable cytokine gene-modified tumor infiltrating lymphocyte (TIL) therapy for metastatic renal cell carcinoma (mRCC). The cytokine gene modified TIL therapy can be applied to ovarian cancer, lung cancer, melanoma and many other human malignancies. The rationale for initially targeting mRCC is as follows.

First, mRCC is poorly responsive to most chemotherapeutic drugs, hormones and radiation therapy. While immunotherapy is promising, the relatively low response rate and the limiting toxicity of immunotherapy regimens stress the need to develop new therapeutic modalities. Second, a tetracycline-responsive recombinant adenovirus vector, AdVtTA.TNFα, has been generated. Human and murine T-lymphocytes infected with AdVtTA.TNFα secreted high-titer, biologically active TNFα, and the expression of TNFα in the host cell can be reversibly turned on and off (Example 7). Third, although it has been questioned whether specific CTL play an important role in tumor regression in patients with RCC who receive immunotherapy, more recent studies demonstrated that RCC-specific CTL do exist (Koo *et al.*, 1991; Finke *et al.*, 1992; Schendel and Gansbacher, 1993; Schendel *et al.*, 1993).

Fourth, preincubation of RCC tumor cells with IFN-γ, IFN-α and/or TNF-α significantly enhanced susceptibility to lysis by autologous TIL (Schendel *et al.*, 1993; Stotter *et al.*, 1989). In fact, many cytolytic and non-cytolytic $CD8^+$ TIL cultures specifically secreted IFNs and TNF-α when stimulated with tumor cells *in vitro* (Wang *et al.*, 1995; Finke *et al.*, 1994). The effectiveness of TIL when adoptively transferred to mice bearing micrometastases correlated even better with their ability to secrete these specific cytokines than with their apparent cytotoxicity *in vitro* (Finke *et al.*, 1994; Barth *et al.*, 1991).

A. Generation of Regulatable IFN Recombinant Adenoviral Vectors

For these studies, additional adenoviral vectors with tetracycline-regulatable IFN-γ and IFN-α expression are generated using the modified tetracycline-responsive gene expression system. The human and murine IFN-α and IFN-γ cDNA plasmids are readily available from ATCC and R & D System (Minneapolis, MN). Because of the transient nature of the adenovirus-mediated recombinant gene expression, the system is expected to work well for cytokine gene transfer for cancer therapy.

There is now a tetracycline activation (the reverse tet, or tet-on) system in the literature (Gossen *et al.*, 1995). This system, in providing positive activation of gene expression, may have certain advantages for the control of gene expression *in vivo*. A single-plasmid tet-on system will be constructed from EC1214A by replacing the tTA with rtTA (Example 3). The tet-on plasmid with no squelching effects on host cell growth may be used to generate tet-on recombinant cytokine adenovirus vectors.

B. Gene-modified TIL therapy of Murine Renal Adenocarcinoma in Syngeneic Mice

The Renca renal adenocarcinoma model of spontaneous lung metastasis in syngeneic BALB/c mice has been well documented (Murphy and Hrushesky, 1973; Salup and Wiltrout, 1986; Sayers *et al.*, 1990; Golumbek *et al.*, 1991; Dinney *et al.*, 1991; Dinney *et al.*, 1992). To begin with, a 0.05-ml Renca cell suspension containing 10^4 viable cells are injected via a 30-G needle inserted from the lower pole to just below the capsule on the superior pole of the kidney and nephrectomy of the injected kidney is performed 10 days following injection. This protocol results in a 100% incidence of spontaneous lung metastasis of moderate tumor burdens (Dinney *et al.*, 1991; Dinney *et al.*, 1992).

It was reported that mice immunized with Renca cells expressing exogenous IL-4 developed systemic immunity to the parental tumor. This systemic immunity was Renca tumor cell-specific and primarily mediated by $CD8^+$ T cells (Golumbek *et al.*, 1991). Therefore, syngeneic BALB/c mice are challenged subcutaneously with parental Renca tumor cells, followed by immunization with Renca cells engineered to secrete IL-4. Since the murine IL-4 cDNA plasmid is readily available (R & D System, Minneapolis, MN), it is convenient to obtain

stable IL-4-expressing Renca cells for immunization through plasmid transfection. The $CD8^+$ TIL will be separated from the *s.c.* Renca tumors by using immunomagnetic beads (Dynal, Lake Success, NY), and are expanded in low-dose (10 U/ml) human rIL-2 with periodical *in vitro* stimulation with lethally irradiated Renca tumor cells and syngeneic mouse splenocytes. These conditions shall result in TIL with specific cytolytic activity *in vitro*, improved expansion and an increase in cells with substantial functional longevity *in vivo* as compared to TIL grown in high-dose IL-2 (Barth *et al.*, 1990; Chou *et al.*, 1988; Alexander and Rosenberg, 1990; Yang *et al.*, 1990).

The $CD8^+$ TIL obtained in this way are infected with Tc-regulatable adenovirus vectors expressing either TNFα or IFNs, or with multiple vectors in various combinations, in the presence of 0.1μg/ml of Tc. The high-titer adenoviral stocks generated (~$1x10^{11}$ pfu/ml) enable transduction of nearly 100% of the murine TIL (Nakamura *et al.*, 1994; Abe *et al.*, 1996; and Example 7 above). Before adoptive transfer, the transduced $CD8^+$ TIL will be assessed *in vitro* by IL-2 dependent growth, Renca tumor cell-specific cytolytic effect, and their ability and persistency to express the desired cytokines in a Tc-regulatable manner. The cytokine gene-modified TIL will also be examined for homing pattern, persistency and regulatable cytokine expression in syngeneic BALB/c mice in the presence or absence of Renca tumor challenge. Of note, the target gene expression was regulatable up to six orders of magnitude in mice by changing the doxycycline supply in drinking water.

In this tumor model, spontaneous lung metastases are well established by the time the kidney with local tumors is resected, and adoptive transfer of cytokine gene modified TIL commences one day following nephrectomy. Since host antitumor responses to TIL engineered to secrete TNFα and/or IFNs will be assessed, the conventional preirradiation and systemic administration of exogenous IL-2 following adoptive transfer will be considered only an alternative approach. On day ~35 or when the mice become moribund, animals are ear-tagged, randomized and then sacrificed. The mice are examined for regional and distant disease. The number of lung metastases is determined in a blinded, coded fashion using a dissecting microscope.

Various statistical analyses will be applied to the numbers of metastases, percentages of mice without detectable tumor *versus* days post therapy, and/or survival. For TNF gene-modified TIL therapy, criteria for evaluation of the efficacy also include: 1) determination of TNFα specific effects, by determining if the effect is inhibited by *in vivo* administration of anti-TNF mAbs or by turning off the TNFα expression; and 2) is the effect dependent on cellular immunity (does immune-depletion with anti-CD8 mAbs permit tumor growth). The same criteria can be applied to assessment of IFNs gene-modified TIL therapy (Marincola *et al.*, 1994). The studies are designed to ultimately determine whether adoptive transfer of the TNFα and/or IFNs gene-modified TIL are more effective than non-gene-modified adoptive cellular immunotherapy.

C. Gene-modified TIL therapy of Human Renal Adenocarcinoma in *scid* Mice

The severe combined immune deficient (*scid*) mice offer the possibilities of examining the interaction between human lymphocytes and human tumors (Bankert *et al.*, 1989; Phillips *et al.*, 1989; Williams *et al.*, 1992; Jicha *et al.*, 1992; Williams *et al.*, 1993; Williams *et al.*, 1996). The most important difference between *scid* and *nude* mice is that human TIL can be engrafted and maintained in *scid* mice, but not in nude mice following subcutaneous implantation of fresh tumor biopsy tissue (Williams *et al.*, 1996). In some earlier studies, failure of the isolated TIL to engraft in *scid* mice could have been due in part to the damage of the normal histologic architecture of the tumor and TIL interface, to which TIL are tethered, or due to a complete lack of autologous tumor challenge in the animal (Williams *et al.*, 1996; Volpe *et al.*, 1993). Limitations and variability do exist in the use of the *scid* mice, since significant antitumor response could be elicited from residual host immune effector cells (*e.g.*, NK cells). Therefore, studies designed to elicit human antitumor responses from *scid* mice coengrafted with human lymphocytes must also consider the response from the residual effector cells in the *scid* host (Zhai *et al.*, 1992).

For the purpose of this study, the double-mutant C.B-17-*scid*-beige mice which are deficient in B, T and NK cells will be engrafted with human mRCC tumor tissue. Strict procedures will be observed to maintain the sterility of the tissue from resection to implantation into *scid* mice. Since co-engrafted lymphocytes may prevent tumor growth, 1 to 2 mm^3 pieces of minced fresh tumor (Williams *et al.*, 1996) or single cell suspensions are depleted of TIL by

incubation with anti-CD45 mAb, followed by Dynabeads coated with anti-mouse IgG mAb (Volpe *et al.*, 1993). The supernatant containing tumor pieces or single tumor cells are then injected subcutaneously into *scid* mice. Alternatively, tumor tissues normalized in *nude* mice, bereft of the passenger lymphocytes, can be re-xenografted into *scid* mice (Williams *et al.*, 1996). In the meantime, bulk TIL will be isolated from the fresh autologous tumor, and expanded *in vitro*. The methods and design for TIL isolation, expansion, cytokine gene modification and therapy are similar between the *scid* mouse model and the Renca syngeneic mouse model as described above. The focus of the *scid* mouse model, however, will be placed on ectopic (subcutaneous) tumors. These studies should provide more direct information regarding the efficacy of TNFα and/or IFNs gene-modified human TIL therapy for human renal cancer.

EXAMPLE 12

Tetracycline-Regulatable Human TNF-α Gene Expression

Tumor necrosis factor (TNF-α) is a multifunctional cytokine with direct antitumor activity. Clinical trials using TNF-α for cancer treatment have been disappointing, in part due to its severe side effects, and it has been estimated that TNF-α therapy would be effective only at 5-25 times the maximum tolerated dose. A Tc-responsive recombinant adenovirus vector, AdVtTA.TNF-α has been developed (see Example 7, above). A variety of human tumor cells and T-lymphocytes transduced by AdVtTA.TNF-α secreted high-titer (5,000 to 100,000 pg/10^6 cells/24 h) and biologically active TNF-α in the absence of tetracycline. Expression of TNF-α in the transduced cells was non-detectable when the culture medium contained as low as 0.1 μg/ml of Tc. At least a fraction of the clonogenic cells from human peripheral blood stem cell concentrates were also transducible by AdVtTA.TNF-α. The availability of this type of adenovirus vectors opens a door to tumor- or organ-specific delivery of high-dose TNF-α and potentially also other therapeutic gene products for systemic cancer gene therapy.

A. Materials and Methods

Cell Lines and Human Peripheral Blood Stem Cells. The adenovirus (Ad5) DNA-transformed human embryonic kidney cell line 293, human bladder carcinoma cell line 5637, human prostate carcinoma cell lines DU145 and LNCaP.FGC, human mature T cell line HuT 78,

mouse fibroblast cell line NCTC clone 929 (L929), and mouse cytotoxic T cell line CTLL-2 were obtained from American Type Culture Collection. Human normal peripheral blood stem cell concentrates were collected by standard cytapheresis procedures from patients with underlying urothelial cancers.

Plasmids. The E1 shuttle plasmid pΔE1sp1A and the Ad5 master plasmid pBHG10 were purchased from Microbix Biosystems Inc. The pE4 plasmid containing the complete coding region of the human TNF-α cDNA was obtained from ATCC.

Human TNF-α Assays. The relative mass values for human recombinant TNF-α secreted by AdVtTA.TNF-α-transduced cells in culture were quantitated using human TNF-α ELISA kit according to the technical manual (Sigma, St. Louis, MO). The measurement detects the total amount of TNF-α in tissue culture supernatant, *i.e.*, the total amount of free TNF-α plus the amount of TNF-α bound to soluble receptors.

Bioactivity of TNF-α was measured based on the cytolytic effects of TNF-α on a responsive mouse cell line, L929 (Aggarwal and Kohr, 1985). Briefly, after 3 h of exposure to 1.0 μg/ml of actinomycin D (sensitizer), the L929 cells were treated for 24 h with serial dilutions of the conditioned medium collected from AdVtTA.TNF-α-transduced cell cultures. The numbers of metabolically active cells left in the microtiter plates were determined by 3-(4,5-dimethylthiazol-2yl)-2,5-diphenyl tetrazolium bromide (MTT)-based colorimetric assay (Cell Proliferating Kit I, Boehringer Mannheim).

Expansion of the Hematopoietic Progenitor Cells and Colony Assay. Fresh peripheral blood stem cell concentrates from cytapheresis were treated with ammonium chloride hemolysis solution (0.83% NH_4Cl, 0.1% $NaHCO_3$ and 0.04% Na_2EDTA, pH 7.3) by adding 3 ml solution to 1 ml of the cell suspension to remove red blood cells. The nucleated cells were then grown in IMDM medium containing 20% FBS, 10 ng/ml each of hIL-1α, hIL-3, hIL-6 and stem cell factor (Sigma) (Muench *et al.*, 1994) for about one wk. After *ex vivo* expansion, a portion of the mononuclear cell suspension was infected with the recombinant AdVtTA.TNF-α adenovirus at a multiplicity of infection (MOI) of 100 for 60 min. Colony assay of hematopoietic progenitor cells was performed in methylcellulose medium (Stem Cell Technology Inc.) according to the

technical manual. At day 14, the colonies formed in methylcellulose culture were removed individually using a Pasteur pipette. The removed cells were subjected to RNA extraction and RT-PCR™ analysis for evidence of adenoviral vector-derived TNF-α transcripts.

RNA Extraction and RT-PCR™ Analysis. Total RNA was prepared by RNeasy™ RNA extraction kit (Qiagen) from hematopoietic progenitor colonies. All RNA samples were treated with RNase-free DNase (Invitrogen, San Diego, CA) to remove residual genomic DNAs prior to RT- PCR™ analysis. For detection of adenoviral vector-derived TNF-α transcripts, the initial reverse transcriptase reaction products were subjected two rounds of PCR™ amplification using two sets of oligonucleotide primers. The first set of primers (sense primer 5′-GACAAGCCTGTAGCCCATGTT-3′ (SEQ ID NO:XX) and antisense primer 5′-GGTTACAAATAAAGCAATAGCAT-3′) (SEQ ID NO:XX) for RT- PCR™ amplification spanned a ~700 bp DNA fragment from the 5′-moiety of the TNF-α cDNA insert to the vector-specific SV40 polyadenylation signal sequence. The second set of primers (sense primer 5′-GTAGCAAACCCTCAAGCTGAG-3′ ;SEQ ID NO:XX and antisense primer 5′-CACTGCATTCTAGTTGTGGTT-3′; SEQ ID NO:XX) were nested within the segment amplified by the first set of primers. RT- PCR™ was performed using Titan™ RT- PCR™ System (Boehringer Mannheim).

B. Results

Generation of the recombinant AdVtTA.TNF-α adenovirus vector. Recently, control elements of the tetracycline-resistance operon encoded in transposon Tn10 of *Escherichia coli* have been utilized to establish an efficient Tc-regulated gene expression system in mammalian cells (Gossen and Bujard, 1992). This original multiple-plasmid system has been further modified (see Example 7, above). The modification warrants lower constitutive expression of the tTA transactivator, and therefore eliminates the squelching effect of its activating domain (a portion of the herpes simplex virus VP-16 protein) on host cell growth (Gill and Ptashne, 1988). The modified system is now contained within a single plasmid and is readily convertible to Tc-controlled adenovirus vectors.

Detailed procedures for construction of the AdVtTA.TNF-α adenovirus vector are discussed in Example 7, above. Briefly, both the modified tTA expression cassette and the

tetracycline-responsive TNF-α expression cassette were inserted into the E1 shuttle plasmid pΔE1sp1A which retains the Ad5 packaging signal sequence. The resultant recombinant shuttle plasmid pΔE1.tTA.TNF-α and the Ad5 master plasmid, pBHG10 were then co-transfected into 293 cells in 24-well tissue culture plates *via* Lipofectin (Life Technologies, Inc., Gaithersburg, MD). The pBHG10 plasmid contains the backbone of the circular Ad5 genome with partial deletion of both E1 (0.5-3.7 m.u.) and E3 (77.5-86.2 m.u.) sequences. The E1 deletion in pBHG10 removes the packaging signal. Co-transfection of 293 cells with plasmids pΔE1.tTA.TNF-α and pBHG10 produced infectious virions by *in vivo* recombination, in which the Ad5 packaging signal sequence, the modified tTA expression cassette and the tetracycline-responsive TNF-α expression cassette were rescued into the E1 deletion region (1.0-9.8 m.u.) of the Ad5 genome.

At day 18 after plasmid transfection, presence of infectious adenoviruses as initially demonstrated by cytopathic effect (CPE) was evident in 3 out of 288 wells of 293 cells examined. Cell culture supernatants were collected from the transfected 293 cells in which CPE had occurred. Recombinant viruses were further identified by restriction enzyme digestion mapping and by transducing human cells in culture followed by TNF-α titration under both permissive (medium without tetracycline) and non-permissive (medium containing 0.1 μg/ml tetracycline) conditions. One of the three infectious adenoviruses produced high titers of recombinant TNF-α in a Tc-regulatable manner. The virus was further purified by three rounds of limited dilution of the virus supernatant and designated AdVtTA.TNF-α. Stocks of the AdVtTA.TNF-α (~3x 10^{10} pfu/ml) were prepared by ultracentrifugation banding (Graham and Prevec, 1991; Xu *et al.*, 1996a). Before use, each batch of the adenovirus stocks was evaluated for the absence of replication-competent adenoviruses (Xu *et al.*, 1996a). Of note, initial attempts to generate TNF-α adenovirus vectors using a non-inducible promoter were unsuccessful, most likely because the adenovirus E1a protein normally expressed in the 293 cells sensitizes the cells to the cytotoxic effects of TNF-α (Shisler *et al.*, 1996).

Efficient, Tc-regulated Production of Recombinant Human TNF-α in Various AdVtTA.TNF-α-transduced Human and Mouse Cells. In several types of human tumors tested, the adenovirus vector AdVtTA.TNFα-transduced bladder carcinoma cell line, 5637 and the prostate carcinoma cell line, DU145, produced high titers of TNF-α under permissive condition

(in Tc-free medium) ranging from 6×10^3 to 1×10^5 pg/10^6 cells/24 h (MOI = 100), whereas the leakage expression of TNF-α was very low when the cell culture medium contained as low as 0.1 μg/ml of tetracycline (FIG. 8). The production of TNF-α by AdVtTA.TNFα-transduced cells was vector dose-dependent. The AdVtTA.TNFα-transduced prostate carcinoma cell line LNCaP.FGC, however, secreted only moderated amounts of TNF-α (~400 pg/10^6 cells/24h), at which level the majority of the transduced LNCaP.FGC cells had died. In this connection, it is known that LNCaP is an androgen-dependent cell line that responds to TNF-α in culture by undergoing programmed cell death (Sensibar *et al.*, 1995).

Of importance, the TNF-α production by AdVtTA.TNFα-transduced human mature T lymphocyte cell line, HuT 78, was at the levels of ~5,000 to 10,000 pg/10^6 cells/24h. The HuT 78 has properties of mature T cells with inducer/helper phenotypes and releases IL-2. The non-transduced HuT 78 cells produced undetectable levels of TNF-α, and even at the highest multiplicity of infection examined (MOI=200), the production of TNF-α by AdVtTA.TNFα-transduced HuT 78 cells was readily switched off in culture medium containing 0.1 μg/ml of Tc (FIG. 6). In addition, the AdVtTA.TNFα-infected mouse CTLL-2 T lymphocytes also secreted comparably high levels of human TNF-α in a tetracycline-regulatable manner. CTLL-2 is an IL-2-dependent, cytotoxic T cell line. Thus, in both cases the levels of TNF-α production in hematopoietic cells of the lymphoid lineage were much higher than those which had been shown previously by retroviral vector-mediated TNF-α gene transfer (Marincola *et al.*, 1994; Treisman *et al.*, 1994). The transduced HuT 78 and CTLL-2 T lymphocytes persistently secreted high concentration of TNF-α in Tc-free medium at least for 10 days post-AdVtTA.TNFα infection.

The human TNF-α secreted by AdVtTA.TNFα-transduced tumor cells or T lymphocytes was biologically active. As shown in FIG. 7, Tc-free conditioned media collected from HuT 78 lymphocyte cultures about 4 days after exposure to AdVtTA.TNFα resulted in potent cytolytic effects on actinomycin D-sensitized mouse L929 fibroblast cells. The L929 is a known TNF-α-responsive cell line, and is commonly used for unit definition of biologically active TNF-α. One unit of TNF-α is the amount required to induce half-maximal cytolysis of L929 in the presence of actinomycin D. This approach in combination with the TNF-α ELISA assay determined that the HuT 78 conditioned media tested in FIG. 7 contained ~1×10^5 pg/ml and ~4×10^4 units/ml of TNF-α, or ~4×10^8 units per mg of TNF-α protein.

Transduction of Primary Human Peripheral Blood Stem Cells by AdVtTA.TNFα. To study the use of AdVtTA.TNFα for Tc-regulatable and bone-specific delivery of TNF-α or other cytokines, the effectiveness of AdVtTA.TNFα in transduction of human normal hematopoietic stem cells was studied. The fresh peripheral blood stem cell concentrates collected by cytapheresis contained relatively high numbers of $CD34^+$ cells including pluripotent hematopoietic stem cells but also late committed progenitors already activated *in vivo* by G-CSF or GM-CSF priming (Peters *et al.*, 1993). After *ex vivo* expansion of the peripheral blood progenitors for about 7 days (Muench *et al.*, 1994), aliquots of the nucleated cell suspension were infected with the recombinant AdVtTA.TNF-α adenovirus.

As illustrated in FIG. 9, the AdVtTA.TNF-α was able to transduce the peripheral blood mononuclear cells in a vector dose-dependent manner. The production of recombinant TNF-α was accelerated in Tc-free medium on the second and third day post-infection, reaching the levels of 1,600 to 3,200 pg/10^6 cells/24 h (MOI=100), and was mostly repressed as long as the tissue culture medium contained 0.1 μg/ml of Tc. Of note, the baseline levels of TNF-α expression were also elicited after virus infection. This may represent the endogenous TNF-α secretion from some late committed progenitors and mature blood cell types (such as the activated monocyte and macrophage) in the apheresis samples which was triggered by adenovirus infection.

To determine if the clonogenic hematopoietic progenitors of the peripheral blood were indeed transduced by AdVtTA.TNFα, a colony-forming assay of hematopoietic progenitor cells was performed at 60 min after AdVtTA.TNFα infection. The existence of AdVtTA.TNFα-derived TNF-α transcripts was examined by RT- PCR™ analysis of 10 granulopoietic colonies formed in semi-solid methylcellulose media. The first set of oligonucleotide primers used for the initial PCR™ amplification spanned a chimeric DNA fragment consisting of a large portion of the TNF-α cDNA and the vector-specific SV40 polyadenylation signal sequence. The assay results indicated that ~40% of the colonies contained AdVtTA.TNFα adenovirus-encoded TNF-α transcripts.

In summary, a recombinant adenovirus vector AdVtTA.TNFα was constructed which directed high-level expression of human TNF-α in a Tc-regulatable manner. The AdVtTA.TNFα vector was able to tranduce a variety of tumor cells, cytotoxic and mature T lymphocytes, as well as the hematopoietic stem cells, although in the latter case, the transduction efficiency was relatively low. In this connection, construction of Tc-regulatable AdVtTA.TNFα adenovirus vectors using the backbone of AdPK type adenoviruses, which allow targeting of the virus to broadly expressed heparan-containing cellular receptors and delivery of genes to hematopoietic stem cells and tumor infiltrating lymphocytes at markedly higher efficiencies than unmodified adenovirus vectors (Wickham *et al.*, 1996) holds further promise for tumor- and organ-specific delivery of high-dose therapeutic gene products using genetically modified TIL and hematopoietic stem cells as effector cells.

Additionally, the leakage of TNF-α expression in the replication-competent 293 cells following propagation of the AdVtTA.TNFα adenovirus vector in culture medium containing 0.5 μg/ml Tc was also impressively low. This observation suggests that the Tc-regulatable adenovirus vectors may, in general, facilitate production of various recombinant adenoviruses with insertional gene expression that are highly cytotoxic or cytostatic to the adenovirus producer cells. It should also be a useful approach in many circumstances for improving the quantity (titers) and quality (for example, the ratio of viral particles to plaque-forming units) of the virus supernatant by propagating the adenovirus vectors in 293 producer cells under non-permissive conditions.

EXAMPLE 13

Modification of the RB Protein

A. Construction of RB cDNAs Expressing N-terminal Truncated pRB Proteins

For construction of modified RB cDNAs with various N-terminal deletions, a series of PCR™ primers were designed and synthesized according to the sequences of RB cDNA. The sense primers were determined by the RB cDNA sequences downstream of the deleted N-terminal sequence. All primers contain a *Hin*dIII restriction site (underlined) at the 5'-end and the consensus Kozak cassette (GCCGCC) followed by an ATG (italics). The complete nucleotide sequences of the sense primers are as follows:

5'-CCCAAGCTTGCCGCC*ATG*GAGCAGGACAGCGGCCCGGAC-3' (OMRbSd2-34; SEQ ID NO:16);

5'-CCCAAGCTTGCCGCC*ATG*GATTTTACTGCATTATGTCAG-3' (OMRbSd2-55; SEQ ID NO:17);

5'-CCCAAGCTTGCCGCC*ATG*GAGAAAGTTTCATCTTGTGAT-3' (OMRbSd2-78; SEQ ID NO:18);

5'-CCCAAGCTTGCCGCC*ATG*CTGTGGGGAATCTGTATCTTT-3' (OMRbSd2-97; SEQ ID NO:19);

5'-CCCAAGCTTGCCGCC*ATG*TCAAGACTGTTGAAGAAG-3' (OMRbSd1-147, SEQ ID NO:20).

The anti-sense primer 5'-GTCCAAGAGAATTCATAAAAGG-3' (OMRbAS300; SEQ ID NO:15) overlaps with the *Eco*RI site (underlined) at the nucleotide +900 of the RB cDNA (the A of the first in-frame ATG is designated as position +1). The anti-sense primer was paired with each sense primer described above to amplify various modified 5'-RB cDNA fragments using plasmid F7 as template (which contains the full-length RB cDNA).

After amplification by PCR™ with each pair of primers, the DNA fragments were digested with *Hin*dIII and *Eco*RI and subcloned into plasmid pCMVRB^{110} which had been cut with the same enzymes. The resultant expression plasmids carrying the modified RB cDNAs with N-terminal deletions corresponding to amino acids 2-34, 2-55, 2-78, 2-97 and 1-147 were named as pCMVRBd$_{2\text{-}34}$ (a deletion of amino acids 2 to 34 of the wild type RB protein), pCMVRBd$_{2\text{-}55}$ (a deletion of amino acids 2 to 55 of the wild type RB protein), pCMVRBd$_{2\text{-}78}$ (a deletion of amino acids 2 to 78 of the wild type RB protein), pCMVRBd$_{2\text{-}97}$ (a deletion of amino acids 2 to 97 of the wild type RB protein) and pCMVRBd$_{1\text{-}147}$ (a deletion of amino acids 1 to 147 of the wild type RB protein; amino acid 148 is a methionine) respectively.

B. Construction of RB cDNAs with Internal Deletions or Mutations

A total of seven pRB expression plasmids carrying RB cDNAs with varying internal deletions or mutations have been constructed, namely pCMVRBd$_{31\text{-}107}$ (a deletion of amino acids 31 to 107 of the wild type RB protein), pCMVRBd$_{77\text{-}107}$ (a deletion of amino acids 77 to 107 of the wild type RB protein), pCMVRBm$_{111/112}$ (a mutation of amino acid 111 of the wild type RB protein from aspartic acid to glycine and a mutation of amino acid 112 from glutamic acid to

aspartic acid), pCMVRBd$_{111-181}$ (a deletion of amino acids 111 to 181 of the wild type RB protein), pCMVRBd$_{111-241}$ (a deletion of amino acids 111 to 241 of the wild type RB protein), pCMVRBd$_{181-241}$ (a deletion of amino acids 181 to 241 of the wild type RB protein) and pCMVRBd$_{242-300}$ (a deletion of amino acids 242 to 300 of the wild type RB protein).

For the construction of pCMVRBd$_{31-107}$, an RB cDNA fragment from nucleotide position +325 to +910 was amplified from the plasmid F7 by PCR™ using the primers 5'-GCGCCTGAGGACCTAGATGAGATGTCGTTC-3' (SEQ ID NO:21) and OMRbAS300 (SEQ ID NO:15). This RB cDNA fragment was digested with *Bsu*36I (underlined) and *Eco*RI (from OMRbAS300), and inserted into plasmid pCMVRB^{110} digested with the same enzymes, to replace the original RB cDNA fragment from nucleotides +91 to +900.

For the construction of pCMVRBd$_{77-107}$, an RB cDNA fragment (nucleotides +328 to +910) was amplified from the plasmid F7 by PCR™ using the oligonucleotides 5'-GCGGTTAACCCTAGATGAGATGTCGTTCACT-3' (SEQ ID NO:22) and OMRbAS300 (SEQ ID NO:15), followed by digestion with *Hpa*I (underlined) and *Eco*RI. The amplified, digested fragment was inserted into plasmid pCMVRB^{110} digested with the same enzymes, to replace the RB cDNA fragment from nucleotides +230 to +900.

For the construction of pCMVRBm$_{111/112}$, two pairs of primers were used to change nucleotide A (position +332 of the wild-type RB cDNA) to G, in order to change the codon for aspartic acid (GAT) to glycine (GGT), thus creating a new restriction enzyme site, *Avr*II, and nucleotide G (position +336 of the wild-type RB cDNA) to T, in order to change the codon for glutamic acid (GAG) to aspartic acid (GAT). The first pair of primers are 5'-CCCAAGCTTGCCGTC*ATG*CCGCCCAAAACCCCCCGA-3' (OMRBS1; SEQ ID NO:23) and 5'-CTCACCTAGGTCAACTGCTGCAAT-3' (OMRbAS332; SEQ ID NO:24; the mutated base is in bold). The second pair of primers are 5'-GTTGACCTAGGTGATATGTCGTTC-3' (OMRbS332; SEQ ID NO:25; the mutated bases are in bold) and OMRbAS300 (SEQ ID NO:15). The PCR™ products amplified with OMRBS1 and OMRbAS332 were digested with *Hin*d III and *Avr*II (underlined), and those amplified with OMRbS332 and OMRbAS300 were digested with *Avr*II and *Eco*RI. These fragments were ligated together into plasmid pCMVRB^{110} digested with *Hin*dIII and *Eco*RI to replace the corresponding wild-type RB cDNA sequences.

For the construction of pCMVRBd$_{111\text{-}181}$, the RB cDNA fragment (nucleotides +543 to +910) was amplified from plasmid F7 by PCR™ using the oligonucleotides 5'-GCGCCTAGGATCTACTGAAATAAATTCTGCA-3' (SEQ ID NO:26) and OMRbAS300 (SEQ ID NO:15), followed by digestion with *Avr*II (underlined) and *Eco*RI. This fragment was then ligated into pCMVRBm$_{111/112}$ (above) digested with the same enzymes to replace the RB cDNA fragment from nucleotides +331 to +900.

For the construction of pCMVRBd$_{111\text{-}241}$, a 5' RB cDNA fragment containing nucleotides +1 to +331 was obtained by digestion of pCMVRBm$_{111}$ with *Hin*dIII and *Avr*II. The 3' RB cDNA fragment beginning from nucleotide +722 was isolated from the same plasmid digested with *Pvu*II and *Bam*HI. Then the two DNA fragments (in-frame) were ligated into pCMV-G digested with *Hin*dIII and *Bam*HI.

For the construction of pCMVRBd$_{181\text{-}241}$, a 5'-RB cDNA fragment containing nucleotides +1 to +538 was amplified from plasmid F7 by PCR™ with primers OMRBS1 (SEQ ID NO:23) and 5'-CCCGATATCAACTGCTGGGTTGTGTCAAATA-3' (SEQ ID NO:27) using plasmid F7 as a template. The obtained RB cDNA fragment was cut with *Hin*dIII and *Eco*RV (underlined), and inserted into pCMVRB^{110} to replace the original 5' RB cDNA fragment between the *Hin*dIII and *Pvu*II sites.

For the construction of pCMVRBd$_{242\text{-}300}$, primers OMRBS1 (SEQ ID NO:23) and 5'-CCCGAATTCGTTTTATATGGTTCTTTGAGCAA-3' (SEQ ID NO:28) were used to amplify the 5' RB cDNA fragment containing nucleotides +1 to +722 using plasmid F7 as a template. The amplified product was digested with *Hin*dIII and *Eco*RI (underlined), and inserted into pCMVRB^{110} digested with the same enzymes to replace the original 5' RB cDNA sequences from nucleotides +1 to +900.

C. Characterization of N-terminal Modified RB Proteins

An RB-defective bladder carcinoma cell line, 5637 was transfected with the expression plasmids carrying the modified RB cDNAs driven by a CMV promoter. The biological function of the mutant pRBs was evaluated by a combined technique involving immunocytochemical

staining and [^{3}H]-thymidine *in situ* labeling of the tumor cells after transfection (Xu *et al.*, 1994a; 1994b).

Tumor cells were seeded onto coverslips in medium containing tetracycline and transfected with plasmids expressing pRB^{94}, pRB^{110} or other mutant RB proteins. At specified time point after removal of tetracycline from the culture medium, the cells were incubated with 1 ml of fresh medium containing 10 μCi [^{3}H]-methyl thymidine (Amersham, Arlington Heights, IL) for 2 hours at 37°C, then fixed and immunochemically stained for expression of RB protein as described previously (Xu *et al.*, 1991a; 1991b). Stained slides were subsequently coated with a thin layer of gelatin and dried at 37°C overnight. The slides were then overlaid with autoradiographic emulsion (Type NTB2, Eastman Kodak, Rochester, NY) and exposed for 2 days. After development, slides were examined under a light microscope.. Twenty-four hours after transfection, cells were processed for immunocytochemical staining of RB protein and [^{3}H]-thymidine incorporation assay as described above.

The results are illustrated in Table 6. When up to 55 amino acid residues were deleted from the N-terminal of pRB, the DNA synthesis was not significantly reduced in the cells transfected with the mutant pRB expression plasmids compared to cells expressing the full-length RB protein. However, when another 23 amino acids were removed from the N-terminal, the cellular DNA synthesis was dramatically suppressed by expression of the truncated pRB.

Table 6

	% Cells Incorporating [^{3}H]-Thymidine	
RB Construct	**$RB^{\pm}$**	**RB^{-}**
Wild-Type	14	41
d2-34	12	42
d2-55	11	43
d2-78	3	41
d2-97	3	42
d1-112	2	42
d1-147	4	42
d31-107	3	41

Table 6 (Continued)

RB Construct	% Cells Incorporating [^{3}H]-Thymidine	
	RB^+	RB^-
d77-107	2	40
d111-112	6	40
d111-181	3	38
d111-241	2	40
d111-414	24	42
d181-241	8	43
d242-300	17	43

As demonstrated in Table 6, the pRB mutants with any deletions between amino acid 55 and 181 significantly inhibit DNA synthesis after being introduced into the tumor cells. Of note, cells transfected with pRBs containing deletions between amino acid 181 and 241 showed weaker inhibition of DNA synthesis than those transfected with plasmids expressing pRBs carrying deletions between amino acid 55 and 181, although these were still more effective than cells transfected with the full-length pRB expression plasmid. Additionally, two pRB mutants with two deletions each, either between amino acid 2 and 34 and between amino acids 76 and 112, or between amino acids 2 and 55 and between amino acids 76 and 112 significantly inhibited DNA synthesis as compared to the wild-type RB. The results indicated the boundary of the putative N-terminal domain probably located between amino acid 182 and 300, most probably between amino acid 182 and 241. In addition, a pRB carrying a point mutation at amino acid position 111 converting aspartic acid to glycine significantly suppressed DNA synthesis, further suggesting that this region is vital for regulating pRB function.

EXAMPLE 14

Induction of Senescence and Telomerase Inhibition by Reexpression of RB

Normal human diploid cells senesce *in vitro* and *in vivo* after a limited number of cell divisions. This process, known as cellular senescence, is an underlying cause of aging and a critical barrier for development of human cancers. This Example presents studies that

demonstrate that reexpression of functional pRB alone in *RB/p53*-defective tumor cells *via* a modified tetracycline-regulated gene expression system resulted in a stable growth arrest at the G0/G1 phase of the cell cycle, preventing tumor cells from entering S phase in response to a variety of mitogenic stimuli. These cells displayed multiple morphological changes consistent with cellular senescence and expressed a senescence-associated β-galactosidase biomarker.

Additionally, telomerase activity, which is believed to be essential for an extended proliferative life-span of neoplastic cells, was abrogated or repressed in the tumor cell lines after induction of pRB (but not p53) expression. Strikingly, when returned to an non-permissive medium for pRB expression, the pRB-induced senescent tumor cells resumed DNA synthesis and attempted to divide. However, most cells died in the process, a phenomenon similar to postsenescent crisis of SV40 T-antigen-transformed human diploid fibroblasts in late passage. These observations provide direct evidence that overexpression of pRB alone in *RB/p53*-defective tumor cells is sufficient to reverse their immortality and cause a phenotype that is, by all generally accepted criteria, indistinguishable from replicative senescence. The results indicate that pRB may play a causal role in the intrinsic cellular senescence program.

A. Materials and Methods

Establishing tumor cell lines with Tc-regulatable pRB expression

The original multiple-plasmid tetracycline repressor/operator-based regulatory system was improved as described in detail above. All *RB*-reconstituted tumor cell lines used in this Example were subjected to at least two rounds of subcloning following the initial plasmid transfection and are considered pure clones. The homogeneity of these clones was verified by pRB nuclear staining. In addition, a panel assay (Zhou *et al.*, 1994b) was used to ensure stable expression of the functional pRB under permissive conditions. The *RB*-reconstituted tumor cells were all RB^- in the presence of 0.5 μg/ml of Tc in culture medium; while the great majority (>99%) of the cells became RB^+ at 24 hours after removal of Tc as shown by immunocytochemical staining.

Flow cytometric analysis

Single cell suspensions collected at each time point were fixed with paraformaldehyde and ethanol before propidium iodide (PI) (Sigma) staining. All profiles were generated using a

FACScan flow cytometer (Becton-Dickinson). The first peak (M1) contains cells with diploid DNA in G0/G1, the second peak (M3) with twice the PI-fluorescence intensity contains tetraploid G2/M cells, and the area between the two peaks (M2) represents the total number of cells in S phase (Nicoletti *et al.*, 1991).

SA-β-gal assay

The assay was performed essentially as previously described (Dimri *et al.*, 1995). Briefly, the cells were fixed in 2% formaldehyde/0.2% glutaraldehyde for 5 min and stained with 5-bromo-4-chloro-3-indolyl β-D-galactoside (X-Gal) at pH 6.0 for 6 hours. The staining solution contained 1 mg/ml X-Gal, 40 mM citric acid/sodium phosphate, pH 6.0, 5 mM potassium ferrocyanide, 5 mM potassium ferricyanide, 150 mM NaCl and 2 mM $MgCl_2$.

Telomeric repeat amplification protocol (TRAP) assay

The methodology, according to the technical manual, was modified from the original TRAP assay as described by Kim *et al.* (1994). In short, ~10^6 cells grown in a 100-mm Petri dish were harvested and resuspended in 200 µl of ice-cold lysis buffer for 30 min on ice, followed by centrifugation at 100,000 × g for 30 min at 4°C. The supernatant was diluted to 0.5 µg protein/µl, of which 2µl was used for each TRAP assay. The telomerase reaction was carried out at 30°C for 30 min, which was followed by a 2-step PCR™ amplification with [γ-^{32}P]-labeled TS primer (94°C, 30 s and 60°C, 30 s for 33 cycles). The PCR™-amplified telomerase extension products were subjected to electrophoresis on a 12.5% polyacrylamide gel.

B. Results

pRB-mediated irreversible growth cessation of tumor cells

Using the modified tetracycline (Tc)-regulatable gene expression system as described in detail above, dozens of long-term stable tumor cell clones were established, in which expression of the wild-type pRB can be reversibly turned on and off without significant leakage. The *RB*-reconstituted tumor cell clones were obtained, respectively, from the breast carcinoma cell line, MDA-MB-468, the osteosarcoma cell line Saos-2, and the bladder carcinoma cell line, 5637. These tumor cell lines were chosen as host cells since they were known to contain both *RB* and *p53* gene mutations (Wang *et al.*, 1993; Chen *et al.*, 1990; Berry *et al.*, 1996; Masuda *et al.*, 1987).

As measured by western blotting, pRB protein induced in the tumor cells reached the highest level about 24 hours after removal of tetracycline from the cell culture medium, and then became completely dephosphorylated within 24 to 40 hours. The effects of induction of pRB expression on tumor cell growth were subsequently examined in representative clones by measuring growth curves and (^{3}H) thymidine incorporation (Xu *et al.*, 1994b), and by flow cytometric analysis (Nicoletti *et al.*, 1991). Cell growth and DNA synthesis of all the long-term tumor cell clones studied ceased 24 to 48 hours after pRB expression was induced (FIG. 3A, FIG. 3B and FIG. 3C). The great majority of the tumor cells were arrested at G0/G1 phase of the cell cycle.

After a 4-day induction of pRB expression in Tc-free medium, the growth cessation of the tumor cells was irreversible by stimulation with a variety of mitogens, such as serum growth factors, phytohemagglutinin (PHA) and concanavalin A (Con A). This was determined by continuous flat growth curves as shown in FIG. 3A, FIG. 3B and FIG. 3C and failure of the tumor cells to incorporate (^{3}H) thymidine in response to mitogenic stimulation. In the meantime, the tumor cells displayed striking morphological changes consistent with cellular senescence, including cell enlargement, flattening, and lower nucleocytoplasmic ratio than cycling cells.

Furthermore, as measured by DNA fragmentation assay, a small amount of lower molecular weight DNAs were often observed in DNA samples prepared from *RB*-reconstituted Saos-2 tumor cells grown in non-permissive but not permissive conditions for pRB expression. This finding suggested a low level of spontaneous apoptosis of the *RB*-defective tumor cell culture, which was inhibited by induction of pRB expression. In addition, switching on pRB expression in the *RB*-reconstituted 5637 and MDA-MB-468 tumor cell lines also inhibited IFN-γ-induced apoptotic cell death.

Expression of senescence-associated β-*galactosidase*

A biomarker that identifies senescent human cells in culture and in aging skin *in vivo* has recently been reported. This marker, termed senescence-associated β-galactosidase (SA-β-gal), is expressed by senescent, but not pre-senescent fibroblasts. SA-β-gal was also absent from immortal cells but was induced by genetic manipulations that reversed immortality (Dimri *et al.*,

1995). Young (early passage) human WI-38 fibroblasts were SA-β-gal negative, whereas the senescent (at population doubling level greater than 52) WI-38 cells were strongly SA-β-gal positive, which provided a valid control for the SA-β-gal assay. The Tc-responsive *RB*-reconstituted tumor cell clones were totally SA-β-gal negative in the presence of Tc (*i.e.*, in RB^- status), and the majority of the tumor cells became SA-β-gal positive after induction of pRB expression for four to five days in Tc-free medium. The detection of this senescence-associated biomarker in the tumor cells was coincident with the irreversible growth cessation of the tumor cell populations (FIG. 3A, FIG. 3B and FIG. 3C). The intensity of the SA-β-gal staining of the induced RB^+ tumor cells, however, was variable depending on the tumor cell types.

Reexpression of pRB (but not p53) in tumor cells inhibited telomerase activity

Since telomerase has recently emerged as an attractive candidate for a regulator in cellular senescence (Linskens *et al.*, 1995; Klingelhutz *et al.*, 1996), the effects of pRB and p53 replacement on the telomerase activity of the host tumor cells were determined. In this connection, several long-term stable tumor cell clones with Tc-regulatable wild-type p53 expression from the osteosarcoma cell line, Saos-2 were established. A telomeric repeat amplification protocol (TRAP) assay as recently described (Kim *et al.*, 1994) was used to measure telomerase activity in tumor cells before and after induction of pRB (or p53) expression.

Prior to induction of pRB expression, the *RB*-reconstituted tumor cell clones from all three *RB/p53*-defective tumor types examined were positive for telomerase activity, whereas the relative telomerase activity was ~15 to >100 times lower in the tumor cells after turning on the pRB expression as estimated by densitometry of the digitized image. In fact, the telomerase activity was nearly non-detectable in the pRB-expressing MDA-MB-468 and Saos-2 tumor cells. In contrast, although induction of wild-type p53 expression in Saos-2 did result in growth arrest of the $RB^-/p53^{null}$ tumor cells, the p53-reconstituted Saos-2 tumor clones persistently exhibited positive telomerase activity, which was not affected by their p53 status. Thus the differences in telomerase activity cannot be explained simply as a difference in cell proliferation.

Postsenescent crisis of pRB-induced senescent tumor cells after withdrawal of pRB

The pRB-induced tumor cell senescence was stringently dependent on the continued expression of the functional pRB. As shown above, after induction of pRB expression in Tc-free

medium for four or more days, the *RB*-reconstituted MDA-MB-468, Saos-2, and 5637 tumor cells became senescent. When these tumor cells returned to an non-permissive medium for pRB expression, however, a large number of tumor cells were observed that lost cell-cell adherence, detached from the Petri dishes and died. To further characterize this phenomenon, a combined method was employed involving pRB immunocytochemical staining and (^{3}H) thymidine *in situ* labeling of the tumor cells.

It was found that after adding 0.5 μg/ml of Tc back to the *RB*-reconstituted Saos-2 tumor cell cultures that had been maintained in Tc-free medium for 4 to 5 days, nearly all tumor cells were depleted of the exogenous pRB and became RB$^-$ at day 6. Subsequently, at day 9 to 10, the tumor cells resumed DNA synthesis, the majority of which however had strikingly aberrant nuclei. They attempted to divide but most died in the process. These tumor cells displyed a phenotype, showing remarkable similarity to postsenescent crisis of the T-antigen-transformed human cells in late passage (Stein, 1985).

In summary, reexpression of functional pRB in *RB*-defective tumor cells induced growth cessation concurrently with inhibition of telomerase activity. The tumor cells irreversibly lost mitogen responsiveness, entering a viable G1-arrested state. They also exhibited pRB-dependent SA-β-gal positivity (a senescence-associated biomarker) and resistance to apoptotic cell death. Of note, replacement of either wild-type pRB or p53 in the RB$^-$/p53^{null} Saos-2 was able to block tumor cell growth at the population level, but only pRB induced inhibition of telomerase. Furthermore, withdrawal of pRB in pRB-induced senescent tumor cells led to a crisis-like phenotype. These observations, taken together, suggest pRB is causally involved in the cellular senescence program. These results are the first direct evidence that overexpression of pRB alone in a variety of *RB*-defective tumor cells was sufficient to reverse their immortality and cause *bona fide* replicative senescence. Since all three *RB*-defective tumor cell lines examined also have p53 mutations, the pRB-mediated tumor cell senescence apparently do not require wild-type p53 function.

Thus a new link between pRB and telomeraseis shown. It is demonstrated, by a telomeric repeat amplification protocol (TRAP) assay, that reexpression of pRB in *RB*-defective tumor cells inhibits telomerase activity. Because of the high sensitivity of the polymerase chain

reaction (PCR™)-based TRAP assay, which detects the enzyme activity in a very small number of telomerase positive cells, and the difficulty in obtaining absolutely pure *RB*-reconstituted cell clones, the effectiveness of pRB reexpression on inhibition of telomerase activity in *RB*-defective tumor cells was likely even greater than it had been detected by the *in vitro* assay.

It is also noteworthy that, when maintained in non-permissive conditions for pRB (or p53) expression, the pRB-reconstituted Saos-2 clone apparently had much lower telomerase activity than the p53-reconstituted Saos-2 clone. The difference implies that, even before switching-on of the pRB expression in Tc-free medium, there must be low baseline expression of pRB from the Tc-responsive promoter in Saos-2 cells (Gossen and Bujard, 1995). The leakiness of pRB in pRB-reconstituted tumor cells under non-permissive conditions is below the immunodetection threshold for pRB protein (Xu *et al.*, 1991b), but it might be sufficient to inhibit the most telomerase activity. Since the tumor cells lacking telomerase activity likely resume telomere decline, this would eventually trigger the intrinsic cellular senescence program if it remains intact in the tumor cells.

EXAMPLE 15

Therapeutic Administration of Modified RB Constructs

1. Treatment of Human Bladder Cancers *in vivo*.

The human bladder cancer represents an ideal model for practicing tumor suppressor gene therapy of solid tumors by infusing the instant modified RB protein expression retroviral vectors into the bladder. The original experimental model of human bladder cancer was established by Jones and colleagues (Ahlering *et al.*, 1987). It has been shown that human bladder tumor cells of RT4 cell line established from a superficial papillary tumor, which usually does not metastasize, produced tumors only locally when injected by a 22-gauge catheter into the bladder of female nude mice. In contrast, the EJ bladder carcinoma cells which were originally isolated from a more aggressive human bladder cancer produced invasive tumors in the nude mouse bladders which metastasized to the lung spontaneously. Therefore, this model can be used for treatment of experimental bladder cancer by *in vivo* gene transfer with retroviral vectors.

Tumor cells from RB minus human bladder carcinoma cell line, 5637 (ATCC HTB9) and RB^+ human bladder carcinoma cell line, SCaBER (ATCC HTB3) will be injected directly into the bladders of female athymic (nu/nu) nude mice (6 to 8 weeks of age) by a catheter as initially reported by Jones and colleagues (Ahlering *et al.*, 1987). Development and progression of the nude mouse bladder tumors will be monitored using a fiber-optical system to which a TV monitor is attached. The experimental tumors will subsequently be treated with retrovirus vectors of the present invention expressing the modified RB proteins.

Supernatants with high virus titers will be obtained from tissue culture media of selected clones expressing high level of human modified RB protein and confirmed as free of replication-competent virus prior to use. The retroviral vector suspension at high titers ranging from 4×10^4 to greater than 1×10^7 colony-forming unit (cfu)/ml, and more preferably at a titer greater than 1×10^6 cfu/ml will then be infused directly into the mouse bladders *via* a catheter to treat the tumors. The skilled artisan will understand that such treatments may be repeated as many times as necessary *via* a catheter inserted into the bladder. The tumor regression following transferring the modified RB gene will be monitored frequently *via* the fiber-optic system mentioned above.

The same procedure as described above may be used for treating the human bladder cancer except that the retroviral vector suspension is infused into a human bladder bearing cancer.

2. *in vivo* Studies Using an Orthotopic Lung Cancer Model

Human large cell lung carcinoma, NCI-H460 (ATCC HTB177) cells which have normal pRB^{110} expression will be injected into the right mainstream bronchus of athymic (nu/nu) nude mice (10^5 cells per mouse). Three days later the mice will be inoculated endobronchically with supernatant from the modified RB, or wild-type RB retrovirus producer cells daily for three consecutive days. Tumor formation suppression in the group of mice treated with the modified RB retrovirus supernatant, in contrast, to the group which is treated with wild-type RB retrovirus supernatant, will indicate that the modified RB-expressing retrovirus inhibits growth of RB^+ non-small cell lung carcinoma (NSCLC) cells, whereas the wild-type RB-expressing retrovirus does not.

3. Treatment of Human N n-Small Cell Lung Cancers *in vivo.*

Non-small cell lung cancer patients having an endobronchial tumor accessible to a bronchoscope, and also having a bronchial obstruction, will be initially selected for modified RB gene therapy. Treatment will be administered by bronchoscopy under topical or general anesthesia. To begin the procedure, as much gross tumor as possible will be resected endoscopically. A transbronchial aspiration needle (21G) will be passed through the biopsy channel of the bronchoscope. The residual tumor site will then be injected with the appropriate modified RB retroviral vector supernatant, modified RB adenovirus suspension or modified RB-expressing plasmid vector-liposome complexes at a volume of 5 ml to 10 ml. Protamine may be added to a concentration of 5 μg/ml. The injections of therapeutic viral or plasmid supernatant comprising one or more of the vectors will be administered around and within the tumor or tumors and into the submucosa adjacent to the tumor. The injections will be repeated daily for five consecutive days and monthly thereafter. The treatment may be continued as long as there is no tumor progression. After one year the patients will be evaluated to determine whether it is appropriate to continue therapy.

In addition, as a precaution, the patients will wear a surgical mask for 24 hours following injection of the viral supernatant. All medical personnel will wear masks routinely during bronchoscopy and injection of the viral supernatant. Anti-tussive will be prescribed as necessary.

4. Treatment or Prevention of Human Lung Carcinomas With Liposome-Encapsulated Purified Modified RB Protein

In yet another alternative, target tumor or cancer cells will be treated by introducing the modified RB proteins into cells in need of such treatment by any known method. For example, liposomes are artificial membrane vesicles that have been extensively studied for their usefulness as delivery vehicles of drugs, proteins and plasmid vectors both *in vitro* or *in vivo* (Mannino *et al.*, 1988). Proteins such as erythrocyte anion transporter (Newton *et al.*, 1988), superoxide dismutase and catalase (Tanswell *et al.*, 1990), and UV-DNA repair enzyme (Ceccoli *et al.*, 1989) have been encapsulated at high efficiency with liposome vesicles and delivered into mammalian cells *in vitro* or *in vivo*. Further, small-particle aerosols provide a method for the delivery of drugs for treatment of respiratory diseases. For example, it has been reported that

drugs can be administered in small-particle aerosols by using liposomes as a vehicle. Administered *via* aerosols, the drugs are deposited rather uniformly on the surface of the nasopharynx, the tracheobronchial tree and in the pulmonary area (Knight *et al.*, 1988).

To treat or prevent lung cancers, the therapeutic modified RB proteins will be purified, for example, from recombinant baculovirus AcMNPV-modified RB infected insect cells by immunoaffinity chromatography or any other convenient source. The modified RB protein will then be mixed with liposomes and incorporated into the liposome vesicles at high efficiency. The encapsulated modified RB will still be active. Since the aerosol delivery method is mild and well-tolerated by normal volunteers and patients, the modified RB-containing liposomes can be administered to treat patients suffering from lung cancers of any stage and/or to prevent lung cancers in high-risk population. The modified RB protein-containing liposomes may administered by nasal inhalation or by a endotracheal tube *via* small-particle aerosols at a dose sufficient to suppress abnormal cell proliferation. Aerosolization treatments will be administered to a patient for 30 minutes, three times daily for two weeks, with repetition as needed. The modified RB protein will thereby be delivered throughout the respiratory tract and the pulmonary area. The treatment may be continued as long as necessary. After one year, the overall condition of the patient will be evaluated to determine if continued therapy is appropriate.

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All of the compositions and methods disclosed and claimed herein can be made and executed without undue experimentation in light of the present disclosure. While the compositions and methods of this invention have been described in terms of preferred embodiments, it will be apparent to those of skill in the art that variations may be applied to the compositions and methods, and in the steps or in the sequence of steps of the methods described herein without departing from the concept, spirit and scope of the invention. More specifically, it will be apparent that certain agents which are both chemically and physiologically related may be substituted for the agents described herein while the same or similar results would be achieved. All such similar substitutes and modifications apparent to those skilled in the art are deemed to be within the spirit, scope and concept of the invention as defined by the appended claims.

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(i) APPLICANT:
(A) NAME: Board of Regents, University of Texas System
(B) STREET: 201 W. 7th
(C) CITY: Austin
(D) STATE: Texas
(E) COUNTRY: USA
(F) POSTAL CODE (ZIP): 78701

(ii) TITLE OF INVENTION: VECTORS FOR CONTROLLED GENE EXPRESSION

(iii) NUMBER OF SEQUENCES: 31

(iv) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)

(vi) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: US 60/038,755
(B) FILING DATE: 20-FEB-1997

(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 3555 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION:7..2790

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

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CGCGTC ATG CCG CCC AAA ACC CCC CGA AAA ACG GCC GCC ACC GCC GCC          48
       Met Pro Pro Lys Thr Pro Arg Lys Thr Ala Ala Thr Ala Ala
         1               5                  10

GCT GCC GCC GCG GAA CCC CCG GCA CCG CCG CCG CCG CCC CCT CCT GAG         96
Ala Ala Ala Ala Glu Pro Pro Ala Pro Pro Pro Pro Pro Pro Pro Glu
 15                  20                  25                  30

GAG GAC CCA GAG CAG GAC AGC GGC CCG GAG GAC CTG CCT CTC GTC AGG        144
Glu Asp Pro Glu Gln Asp Ser Gly Pro Glu Asp Leu Pro Leu Val Arg
                 35                  40                  45
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CTT GAG TTT GAA GAA ACA GAA GAA CCT GAT TTT ACT GCA TTA TGT CAG        192
Leu Glu Phe Glu Glu Thr Glu Glu Pro Asp Phe Thr Ala Leu Cys Gln
            50                  55                  60

AAA TTA AAG ATA CCA GAT CAT GTC AGA GAG AGA GCT TGG TTA ACT TGG        240
Lys Leu Lys Ile Pro Asp His Val Arg Glu Arg Ala Trp Leu Thr Trp
         65                  70                  75

GAG AAA GTT TCA TCT GTG GAT GGA GTA TTG GGA GGT TAT ATT CAA AAG        288
Glu Lys Val Ser Ser Val Asp Gly Val Leu Gly Gly Tyr Ile Gln Lys
      80                  85                  90

AAA AAG GAA CTG TGG GGA ATC TGT ATC TTT ATT GCA GCA GTT GAC CTA        336
Lys Lys Glu Leu Trp Gly Ile Cys Ile Phe Ile Ala Ala Val Asp Leu
 95                  100                 105                 110

GAT GAG ATG TCG TTC ACT TTT ACT GAG CTA CAG AAA AAC ATA GAA ATC        384
Asp Glu Met Ser Phe Thr Phe Thr Glu Leu Gln Lys Asn Ile Glu Ile
                115                 120                 125

AGT GTC CAT AAA TTC TTT AAC TTA CTA AAA GAA ATT GAT ACC AGT ACC        432
Ser Val His Lys Phe Phe Asn Leu Leu Lys Glu Ile Asp Thr Ser Thr
            130                 135                 140

AAA GTT GAT AAT GCT ATG TCA AGA CTG TTG AAG AAG TAT GAT GTA TTG        480
Lys Val Asp Asn Ala Met Ser Arg Leu Leu Lys Lys Tyr Asp Val Leu
        145                 150                 155

TTT GCA CTC TTC AGC AAA TTG GAA AGG ACA TGT GAA CTT ATA TAT TTG        528
Phe Ala Leu Phe Ser Lys Leu Glu Arg Thr Cys Glu Leu Ile Tyr Leu
    160                 165                 170

ACA CAA CCC AGC AGT TCG ATA TCT ACT GAA ATA AAT TCT GCA TTG GTG        576
Thr Gln Pro Ser Ser Ser Ile Ser Thr Glu Ile Asn Ser Ala Leu Val
175                 180                 185                 190

CTA AAA GTT TCT TGG ATC ACA TTT TTA TTA GCT AAA GGG GAA GTA TTA        624
Leu Lys Val Ser Trp Ile Thr Phe Leu Leu Ala Lys Gly Glu Val Leu
                195                 200                 205

CAA ATG GAA GAT GAT CTG GTG ATT TCA TTT CAG TTA ATG CTA TGT GTC        672
Gln Met Glu Asp Asp Leu Val Ile Ser Phe Gln Leu Met Leu Cys Val
            210                 215                 220

CTT GAC TAT TTT ATT AAA CTC TCA CCT CCC ATG TTG CTC AAA GAA CCA        720
Leu Asp Tyr Phe Ile Lys Leu Ser Pro Pro Met Leu Leu Lys Glu Pro
        225                 230                 235

TAT AAA ACA GCT GTT ATA CCC ATT AAT GGT TCA CCT CGA ACA CCC AGG        768
Tyr Lys Thr Ala Val Ile Pro Ile Asn Gly Ser Pro Arg Thr Pro Arg
    240                 245                 250

CGA GGT CAG AAC AGG AGT GCA CGG ATA GCA AAA CAA CTA GAA AAT GAT        816
Arg Gly Gln Asn Arg Ser Ala Arg Ile Ala Lys Gln Leu Glu Asn Asp
255                 260                 265                 270
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ACA AGA ATT ATT GAA GTT CTC TGT AAA GAA CAT GAA TGT AAT ATA GAT        864
Thr Arg Ile Ile Glu Val Leu Cys Lys Glu His Glu Cys Asn Ile Asp
                275                 280                 285

GAG GTG AAA AAT GTT TAT TTC AAA AAT TTT ATA CCT TTT ATG AAT TCT        912
Glu Val Lys Asn Val Tyr Phe Lys Asn Phe Ile Pro Phe Met Asn Ser
            290                 295                 300

CTT GGA CTT GTA ACA TCT AAT GGA CTT CCA GAG GTT GAA AAT CTT TCT        960
Leu Gly Leu Val Thr Ser Asn Gly Leu Pro Glu Val Glu Asn Leu Ser
        305                 310                 315

AAA CGA TAC GAA GAA ATT TAT CTT AAA AAT AAA GAT CTA GAT GCA AGA       1008
Lys Arg Tyr Glu Glu Ile Tyr Leu Lys Asn Lys Asp Leu Asp Ala Arg
    320                 325                 330

TTA TTT TTG GAT CAT GAT AAA ACT CTT CAG ACT GAT TCT ATA GAC AGT       1056
Leu Phe Leu Asp His Asp Lys Thr Leu Gln Thr Asp Ser Ile Asp Ser
335                 340                 345                 350

TTT GAA ACA CAG AGA ACA CCA CGA AAA AGT AAC CTT GAT GAA GAG GTG       1104
Phe Glu Thr Gln Arg Thr Pro Arg Lys Ser Asn Leu Asp Glu Glu Val
                355                 360                 365

AAT GTA ATT CCT CCA CAC ACT CCA GTT AGG ACT GTT ATG AAC ACT ATC       1152
Asn Val Ile Pro Pro His Thr Pro Val Arg Thr Val Met Asn Thr Ile
            370                 375                 380

CAA CAA TTA ATG ATG ATT TTA AAT TCA GCA AGT GAT CAA CCT TCA GAA       1200
Gln Gln Leu Met Met Ile Leu Asn Ser Ala Ser Asp Gln Pro Ser Glu
        385                 390                 395

AAT CTG ATT TCC TAT TTT AAC AAC TGC ACA GTG AAT CCA AAA GAA AGT       1248
Asn Leu Ile Ser Tyr Phe Asn Asn Cys Thr Val Asn Pro Lys Glu Ser
    400                 405                 410

ATA CTG AAA AGA GTG AAG GAT ATA GGA TAC ATC TTT AAA GAG AAA TTT       1296
Ile Leu Lys Arg Val Lys Asp Ile Gly Tyr Ile Phe Lys Glu Lys Phe
415                 420                 425                 430

GCT AAA GCT GTG GGA CAG GGT TGT GTC GAA ATT GGA TCA CAG CGA TAC       1344
Ala Lys Ala Val Gly Gln Gly Cys Val Glu Ile Gly Ser Gln Arg Tyr
                435                 440                 445

AAA CTT GGA GTT CGC TTG TAT TAC CGA GTA ATG GAA TCC ATG CTT AAA       1392
Lys Leu Gly Val Arg Leu Tyr Tyr Arg Val Met Glu Ser Met Leu Lys
            450                 455                 460

TCA GAA GAA GAA CGA TTA TCC ATT CAA AAT TTT AGC AAA CTT CTG AAT       1440
Ser Glu Glu Glu Arg Leu Ser Ile Gln Asn Phe Ser Lys Leu Leu Asn
        465                 470                 475

GAC AAC ATT TTT CAT ATG TCT TTA TTG GCG TGC GCT CTT GAG GTT GTA       1488
Asp Asn Ile Phe His Met Ser Leu Leu Ala Cys Ala Leu Glu Val Val
    480                 485                 490
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ATG GCC ACA TAT AGC AGA AGT ACA TCT CAG AAT CTT GAT TCT GGA ACA      1536
Met Ala Thr Tyr Ser Arg Ser Thr Ser Gln Asn Leu Asp Ser Gly Thr
495                 500                 505                 510

GAT TTG TCT TTC CCA TGG ATT CTG AAT GTG CTT AAT TTA AAA GCC TTT      1584
Asp Leu Ser Phe Pro Trp Ile Leu Asn Val Leu Asn Leu Lys Ala Phe
                515                 520                 525

GAT TTT TAC AAA GTG ATC GAA AGT TTT ATC AAA GCA GAA GGC AAC TTG      1632
Asp Phe Tyr Lys Val Ile Glu Ser Phe Ile Lys Ala Glu Gly Asn Leu
            530                 535                 540

ACA AGA GAA ATG ATA AAA CAT TTA GAA CGA TGT GAA CAT CGA ATC ATG      1680
Thr Arg Glu Met Ile Lys His Leu Glu Arg Cys Glu His Arg Ile Met
        545                 550                 555

GAA TCC CTT GCA TGG CTC TCA GAT TCA CCT TTA TTT GAT CTT ATT AAA      1728
Glu Ser Leu Ala Trp Leu Ser Asp Ser Pro Leu Phe Asp Leu Ile Lys
    560                 565                 570

CAA TCA AAG GAC CGA GAA GGA CCA ACT GAT CAC CTT GAA TCT GCT TGT      1776
Gln Ser Lys Asp Arg Glu Gly Pro Thr Asp His Leu Glu Ser Ala Cys
575                 580                 585                 590

CCT CTT AAT CTT CCT CTC CAG AAT AAT CAC ACT GCA GCA GAT ATG TAT      1824
Pro Leu Asn Leu Pro Leu Gln Asn Asn His Thr Ala Ala Asp Met Tyr
                595                 600                 605

CTT TCT CCT GTA AGA TCT CCA AAG AAA AAA GGT TCA ACT ACG CGT GTA      1872
Leu Ser Pro Val Arg Ser Pro Lys Lys Lys Gly Ser Thr Thr Arg Val
            610                 615                 620

AAT TCT ACT GCA AAT GCA GAG ACA CAA GCA ACC TCA GCC TTC CAG ACC      1920
Asn Ser Thr Ala Asn Ala Glu Thr Gln Ala Thr Ser Ala Phe Gln Thr
        625                 630                 635

CAG AAG CCA TTG AAA TCT ACC TCT CTT TCA CTG TTT TAT AAA AAA GTG      1968
Gln Lys Pro Leu Lys Ser Thr Ser Leu Ser Leu Phe Tyr Lys Lys Val
    640                 645                 650

TAT CGG CTA GCC TAT CTC CGG CTA AAT ACA CTT TGT GAA CGC CTT CTG      2016
Tyr Arg Leu Ala Tyr Leu Arg Leu Asn Thr Leu Cys Glu Arg Leu Leu
655                 660                 665                 670

TCT GAG CAC CCA GAA TTA GAA CAT ATC ATC TGG ACC CTT TTC CAG CAC      2064
Ser Glu His Pro Glu Leu Glu His Ile Ile Trp Thr Leu Phe Gln His
                675                 680                 685

ACC CTG CAG AAT GAG TAT GAA CTC ATG AGA GAC AGG CAT TTG GAC CAA      2112
Thr Leu Gln Asn Glu Tyr Glu Leu Met Arg Asp Arg His Leu Asp Gln
            690                 695                 700

ATT ATG ATG TGT TCC ATG TAT GGC ATA TGC AAA GTG AAG AAT ATA GAC      2160
Ile Met Met Cys Ser Met Tyr Gly Ile Cys Lys Val Lys Asn Ile Asp
        705                 710                 715
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CTT AAA TTC AAA ATC ATT GTA ACA GCA TAC AAG GAT CTT CCT CAT GCT      2208
Leu Lys Phe Lys Ile Ile Val Thr Ala Tyr Lys Asp Leu Pro His Ala
    720                 725                 730

GTT CAG GAG ACA TTC AAA CGT GTT TTG ATC AAA GAA GAG GAG TAT GAT      2256
Val Gln Glu Thr Phe Lys Arg Val Leu Ile Lys Glu Glu Glu Tyr Asp
735                 740                 745                 750

TCT ATT ATA GTA TTC TAT AAC TCG GTC TTC ATG CAG AGA CTG AAA ACA      2304
Ser Ile Ile Val Phe Tyr Asn Ser Val Phe Met Gln Arg Leu Lys Thr
                755                 760                 765

AAT ATT TTG CAG TAT GCT TCC ACC AGG CCC CCT ACC TTG TCA CCA ATA      2352
Asn Ile Leu Gln Tyr Ala Ser Thr Arg Pro Pro Thr Leu Ser Pro Ile
            770                 775                 780

CCT CAC ATT CCT CGA AGC CCT TAC AAG TTT CCT AGT TCA CCC TTA CGG      2400
Pro His Ile Pro Arg Ser Pro Tyr Lys Phe Pro Ser Ser Pro Leu Arg
        785                 790                 795

ATT CCT GGA GGG AAC ATC TAT ATT TCA CCC CTG AAG AGT CCA TAT AAA      2448
Ile Pro Gly Gly Asn Ile Tyr Ile Ser Pro Leu Lys Ser Pro Tyr Lys
    800                 805                 810

ATT TCA GAA GGT CTG CCA ACA CCA ACA AAA ATG ACT CCA AGA TCA AGA      2496
Ile Ser Glu Gly Leu Pro Thr Pro Thr Lys Met Thr Pro Arg Ser Arg
815                 820                 825                 830

ATC TTA GTA TCA ATT GGT GAA TCA TTC GGG ACT TCT GAG AAG TTC CAG      2544
Ile Leu Val Ser Ile Gly Glu Ser Phe Gly Thr Ser Glu Lys Phe Gln
                835                 840                 845

AAA ATA AAT CAG ATG GTA TGT AAC AGC GAC CGT GTG CTC AAA AGA AGT      2592
Lys Ile Asn Gln Met Val Cys Asn Ser Asp Arg Val Leu Lys Arg Ser
            850                 855                 860

GCT GAA GGA AGC AAC CCT CCT AAA CCA CTG AAA AAA CTA CGC TTT GAT      2640
Ala Glu Gly Ser Asn Pro Pro Lys Pro Leu Lys Lys Leu Arg Phe Asp
        865                 870                 875

ATT GAA GGA TCA GAT GAA GCA GAT GGA AGT AAA CAT CTC CCA GGA GAG      2688
Ile Glu Gly Ser Asp Glu Ala Asp Gly Ser Lys His Leu Pro Gly Glu
    880                 885                 890

TCC AAA TTT CAG CAG AAA CTG GCA GAA ATG ACT TCT ACT CGA ACA CGA      2736
Ser Lys Phe Gln Gln Lys Leu Ala Glu Met Thr Ser Thr Arg Thr Arg
895                 900                 905                 910

ATG CAA AAG CAG AAA ATG AAT GAT AGC ATG GAT ACC TCA AAC AAG GAA      2784
Met Gln Lys Gln Lys Met Asn Asp Ser Met Asp Thr Ser Asn Lys Glu
                915                 920                 925

GAG AAA TGAGGATCTC AGGACCTTGG TGGACACTGT GTACACCTCT GGATTCATTG       2840
Glu Lys

TCTCTCACAG ATGTGACTGT ATAACTTTCC CAGGTTCTGT TTATGGCCAC ATTTAATATC    2900
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TTCAGCTCTT TTTGTGGATA TAAAATGTGC AGATGCAATT GTTTGGGTGA TTCCTAAGCC 2960

ACTTGAAATG TTAGTCATTG TTATTTATAC AAGATTGAAA ATCTTGTGTA AATCCTGCCA 3020

TTTAAAAAGT TGTAGCAGAT TGTTTCCTCT TCCAAAGTAA AATTGCTGTG CTTTATGGAT 3080

AGTAAGAATG GCCCTAGAGT GGGAGTCCTG ATAACCCAGG CCTGTCTGAC TACTTTGCCT 3140

TCTTTTGTAG CATATAGGTG ATGTTTGCTC TTGTTTTTAT TAATTTATAT GTATATTTTT 3200

TTAATTTAAC ATGAACACCC TTAGAAAATG TGTCCTATCT ATCTTCCAAA TGCAATTTGA 3260

TTGACTGCCC ATTCACCAAA ATTATCCTGA ACTCTTCTGC AAAAATGGAT ATTATTAGAA 3320

ATTAGAAAAA AATTACTAAT TTTACACATT AGATTTTATT TTACTATTGG AATCTGATAT 3380

ACTGTGTGCT TGTTTTATAA AATTTTGCTT TTAATTAAAT AAAAGCTGGA AGCAAAGTAT 3440

AACCATATGA TACTATCATA CTACTGAAAC AGATTTCATA CCTCAGAATG TAAAAGAACT 3500

TACTGATTAT TTTCTTCATC CAACTTATGT TTTTAAATGA GGATTATTGA TAGTC 3555

(2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 928 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

Met Pro Pro Lys Thr Pro Arg Lys Thr Ala Ala Thr Ala Ala Ala Ala
1 5 10 15

Ala Ala Glu Pro Pro Ala Pro Pro Pro Pro Pro Pro Pro Glu Glu Asp
20 25 30

Pro Glu Gln Asp Ser Gly Pro Glu Asp Leu Pro Leu Val Arg Leu Glu
35 40 45

Phe Glu Glu Thr Glu Glu Pro Asp Phe Thr Ala Leu Cys Gln Lys Leu
50 55 60

Lys Ile Pro Asp His Val Arg Glu Arg Ala Trp Leu Thr Trp Glu Lys
65 70 75 80

Val Ser Ser Val Asp Gly Val Leu Gly Gly Tyr Ile Gln Lys Lys Lys
85 90 95

Glu Leu Trp Gly Ile Cys Ile Phe Ile Ala Ala Val Asp Leu Asp Glu
100 105 110

Met Ser Phe Thr Phe Thr Glu Leu Gln Lys Asn Ile Glu Ile Ser Val
115 120 125

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His Lys Phe Phe Asn Leu Leu Lys Glu Ile Asp Thr Ser Thr Lys Val
    130                 135                 140

Asp Asn Ala Met Ser Arg Leu Leu Lys Lys Tyr Asp Val Leu Phe Ala
145                 150                 155                 160

Leu Phe Ser Lys Leu Glu Arg Thr Cys Glu Leu Ile Tyr Leu Thr Gln
                165                 170                 175

Pro Ser Ser Ser Ile Ser Thr Glu Ile Asn Ser Ala Leu Val Leu Lys
            180                 185                 190

Val Ser Trp Ile Thr Phe Leu Leu Ala Lys Gly Glu Val Leu Gln Met
        195                 200                 205

Glu Asp Asp Leu Val Ile Ser Phe Gln Leu Met Leu Cys Val Leu Asp
    210                 215                 220

Tyr Phe Ile Lys Leu Ser Pro Pro Met Leu Leu Lys Glu Pro Tyr Lys
225                 230                 235                 240

Thr Ala Val Ile Pro Ile Asn Gly Ser Pro Arg Thr Pro Arg Arg Gly
                245                 250                 255

Gln Asn Arg Ser Ala Arg Ile Ala Lys Gln Leu Glu Asn Asp Thr Arg
            260                 265                 270

Ile Ile Glu Val Leu Cys Lys Glu His Glu Cys Asn Ile Asp Glu Val
        275                 280                 285

Lys Asn Val Tyr Phe Lys Asn Phe Ile Pro Phe Met Asn Ser Leu Gly
    290                 295                 300

Leu Val Thr Ser Asn Gly Leu Pro Glu Val Glu Asn Leu Ser Lys Arg
305                 310                 315                 320

Tyr Glu Glu Ile Tyr Leu Lys Asn Lys Asp Leu Asp Ala Arg Leu Phe
                325                 330                 335

Leu Asp His Asp Lys Thr Leu Gln Thr Asp Ser Ile Asp Ser Phe Glu
            340                 345                 350

Thr Gln Arg Thr Pro Arg Lys Ser Asn Leu Asp Glu Glu Val Asn Val
        355                 360                 365

Ile Pro Pro His Thr Pro Val Arg Thr Val Met Asn Thr Ile Gln Gln
    370                 375                 380

Leu Met Met Ile Leu Asn Ser Ala Ser Asp Gln Pro Ser Glu Asn Leu
385                 390                 395                 400

Ile Ser Tyr Phe Asn Asn Cys Thr Val Asn Pro Lys Glu Ser Ile Leu
                405                 410                 415

Lys Arg Val Lys Asp Ile Gly Tyr Ile Phe Lys Glu Lys Phe Ala Lys
            420                 425                 430
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Ala Val Gly Gln Gly Cys Val Glu Ile Gly Ser Gln Arg Tyr Lys Leu
        435                 440                 445

Gly Val Arg Leu Tyr Tyr Arg Val Met Glu Ser Met Leu Lys Ser Glu
    450                 455                 460

Glu Glu Arg Leu Ser Ile Gln Asn Phe Ser Lys Leu Leu Asn Asp Asn
465                 470                 475                 480

Ile Phe His Met Ser Leu Leu Ala Cys Ala Leu Glu Val Val Met Ala
                485                 490                 495

Thr Tyr Ser Arg Ser Thr Ser Gln Asn Leu Asp Ser Gly Thr Asp Leu
            500                 505                 510

Ser Phe Pro Trp Ile Leu Asn Val Leu Asn Leu Lys Ala Phe Asp Phe
        515                 520                 525

Tyr Lys Val Ile Glu Ser Phe Ile Lys Ala Glu Gly Asn Leu Thr Arg
    530                 535                 540

Glu Met Ile Lys His Leu Glu Arg Cys Glu His Arg Ile Met Glu Ser
545                 550                 555                 560

Leu Ala Trp Leu Ser Asp Ser Pro Leu Phe Asp Leu Ile Lys Gln Ser
                565                 570                 575

Lys Asp Arg Glu Gly Pro Thr Asp His Leu Glu Ser Ala Cys Pro Leu
            580                 585                 590

Asn Leu Pro Leu Gln Asn Asn His Thr Ala Ala Asp Met Tyr Leu Ser
        595                 600                 605

Pro Val Arg Ser Pro Lys Lys Lys Gly Ser Thr Thr Arg Val Asn Ser
    610                 615                 620

Thr Ala Asn Ala Glu Thr Gln Ala Thr Ser Ala Phe Gln Thr Gln Lys
625                 630                 635                 640

Pro Leu Lys Ser Thr Ser Leu Ser Leu Phe Tyr Lys Lys Val Tyr Arg
                645                 650                 655

Leu Ala Tyr Leu Arg Leu Asn Thr Leu Cys Glu Arg Leu Leu Ser Glu
            660                 665                 670

His Pro Glu Leu Glu His Ile Ile Trp Thr Leu Phe Gln His Thr Leu
        675                 680                 685

Gln Asn Glu Tyr Glu Leu Met Arg Asp Arg His Leu Asp Gln Ile Met
    690                 695                 700

Met Cys Ser Met Tyr Gly Ile Cys Lys Val Lys Asn Ile Asp Leu Lys
705                 710                 715                 720

Phe Lys Ile Ile Val Thr Ala Tyr Lys Asp Leu Pro His Ala Val Gln
                725                 730                 735
```

```
Glu Thr Phe Lys Arg Val Leu Ile Lys Glu Glu Glu Tyr Asp Ser Ile
            740                 745                 750

Ile Val Phe Tyr Asn Ser Val Phe Met Gln Arg Leu Lys Thr Asn Ile
        755                 760                 765

Leu Gln Tyr Ala Ser Thr Arg Pro Pro Thr Leu Ser Pro Ile Pro His
    770                 775                 780

Ile Pro Arg Ser Pro Tyr Lys Phe Pro Ser Ser Pro Leu Arg Ile Pro
785                 790                 795                 800

Gly Gly Asn Ile Tyr Ile Ser Pro Leu Lys Ser Pro Tyr Lys Ile Ser
                805                 810                 815

Glu Gly Leu Pro Thr Pro Thr Lys Met Thr Pro Arg Ser Arg Ile Leu
            820                 825                 830

Val Ser Ile Gly Glu Ser Phe Gly Thr Ser Glu Lys Phe Gln Lys Ile
        835                 840                 845

Asn Gln Met Val Cys Asn Ser Asp Arg Val Leu Lys Arg Ser Ala Glu
    850                 855                 860

Gly Ser Asn Pro Pro Lys Pro Leu Lys Lys Leu Arg Phe Asp Ile Glu
865                 870                 875                 880

Gly Ser Asp Glu Ala Asp Gly Ser Lys His Leu Pro Gly Glu Ser Lys
                885                 890                 895

Phe Gln Gln Lys Leu Ala Glu Met Thr Ser Thr Arg Thr Arg Met Gln
            900                 905                 910

Lys Gln Lys Met Asn Asp Ser Met Asp Thr Ser Asn Lys Glu Glu Lys
        915                 920                 925
```

(2) INFORMATION FOR SEQ ID NO: 3:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 3218 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION:7..2454

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

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GCCGTC ATG TCG TTC ACT TTT ACT GAG CTA CAG AAA AAC ATA GAA ATC        48
       Met Ser Phe Thr Phe Thr Glu Leu Gln Lys Asn Ile Glu Ile
         1               5                  10

AGT GTC CAT AAA TTC TTT AAC TTA CTA AAA GAA ATT GAT ACC AGT ACC        96
Ser Val His Lys Phe Phe Asn Leu Leu Lys Glu Ile Asp Thr Ser Thr
 15                  20                  25                  30
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AAA GTT GAT AAT GCT ATG TCA AGA CTG TTG AAG AAG TAT GAT GTA TTG        144
Lys Val Asp Asn Ala Met Ser Arg Leu Leu Lys Lys Tyr Asp Val Leu
                35                  40                  45

TTT GCA CTC TTC AGC AAA TTG GAA AGG ACA TGT GAA CTT ATA TAT TTG        192
Phe Ala Leu Phe Ser Lys Leu Glu Arg Thr Cys Glu Leu Ile Tyr Leu
            50                  55                  60

ACA CAA CCC AGC AGT TCG ATA TCT ACT GAA ATA AAT TCT GCA TTG GTG        240
Thr Gln Pro Ser Ser Ser Ile Ser Thr Glu Ile Asn Ser Ala Leu Val
        65                  70                  75

CTA AAA GTT TCT TGG ATC ACA TTT TTA TTA GCT AAA GGG GAA GTA TTA        288
Leu Lys Val Ser Trp Ile Thr Phe Leu Leu Ala Lys Gly Glu Val Leu
    80                  85                  90

CAA ATG GAA GAT GAT CTG GTG ATT TCA TTT CAG TTA ATG CTA TGT GTC        336
Gln Met Glu Asp Asp Leu Val Ile Ser Phe Gln Leu Met Leu Cys Val
95                  100                 105                 110

CTT GAC TAT TTT ATT AAA CTC TCA CCT CCC ATG TTG CTC AAA GAA CCA        384
Leu Asp Tyr Phe Ile Lys Leu Ser Pro Pro Met Leu Leu Lys Glu Pro
                115                 120                 125

TAT AAA ACA GCT GTT ATA CCC ATT AAT GGT TCA CCT CGA ACA CCC AGG        432
Tyr Lys Thr Ala Val Ile Pro Ile Asn Gly Ser Pro Arg Thr Pro Arg
            130                 135                 140

CGA GGT CAG AAC AGG AGT GCA CGG ATA GCA AAA CAA CTA GAA AAT GAT        480
Arg Gly Gln Asn Arg Ser Ala Arg Ile Ala Lys Gln Leu Glu Asn Asp
        145                 150                 155

ACA AGA ATT ATT GAA GTT CTC TGT AAA GAA CAT GAA TGT AAT ATA GAT        528
Thr Arg Ile Ile Glu Val Leu Cys Lys Glu His Glu Cys Asn Ile Asp
    160                 165                 170

GAG GTG AAA AAT GTT TAT TTC AAA AAT TTT ATA CCT TTT ATG AAT TCT        576
Glu Val Lys Asn Val Tyr Phe Lys Asn Phe Ile Pro Phe Met Asn Ser
175                 180                 185                 190

CTT GGA CTT GTA ACA TCT AAT GGA CTT CCA GAG GTT GAA AAT CTT TCT        624
Leu Gly Leu Val Thr Ser Asn Gly Leu Pro Glu Val Glu Asn Leu Ser
                195                 200                 205

AAA CGA TAC GAA GAA ATT TAT CTT AAA AAT AAA GAT CTA GAT GCA AGA        672
Lys Arg Tyr Glu Glu Ile Tyr Leu Lys Asn Lys Asp Leu Asp Ala Arg
            210                 215                 220

TTA TTT TTG GAT CAT GAT AAA ACT CTT CAG ACT GAT TCT ATA GAC AGT        720
Leu Phe Leu Asp His Asp Lys Thr Leu Gln Thr Asp Ser Ile Asp Ser
        225                 230                 235

TTT GAA ACA CAG AGA ACA CCA CGA AAA AGT AAC CTT GAT GAA GAG GTG        768
Phe Glu Thr Gln Arg Thr Pro Arg Lys Ser Asn Leu Asp Glu Glu Val
    240                 245                 250
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AAT GTA ATT CCT CCA CAC ACT CCA GTT AGG ACT GTT ATG AAC ACT ATC       816
Asn Val Ile Pro Pro His Thr Pro Val Arg Thr Val Met Asn Thr Ile
255                 260                 265                 270

CAA CAA TTA ATG ATG ATT TTA AAT TCA GCA AGT GAT CAA CCT TCA GAA       864
Gln Gln Leu Met Met Ile Leu Asn Ser Ala Ser Asp Gln Pro Ser Glu
                275                 280                 285

AAT CTG ATT TCC TAT TTT AAC AAC TGC ACA GTG AAT CCA AAA GAA AGT       912
Asn Leu Ile Ser Tyr Phe Asn Asn Cys Thr Val Asn Pro Lys Glu Ser
            290                 295                 300

ATA CTG AAA AGA GTG AAG GAT ATA GGA TAC ATC TTT AAA GAG AAA TTT       960
Ile Leu Lys Arg Val Lys Asp Ile Gly Tyr Ile Phe Lys Glu Lys Phe
        305                 310                 315

GCT AAA GCT GTG GGA CAG GGT TGT GTC GAA ATT GGA TCA CAG CGA TAC      1008
Ala Lys Ala Val Gly Gln Gly Cys Val Glu Ile Gly Ser Gln Arg Tyr
    320                 325                 330

AAA CTT GGA GTT CGC TTG TAT TAC CGA GTA ATG GAA TCC ATG CTT AAA      1056
Lys Leu Gly Val Arg Leu Tyr Tyr Arg Val Met Glu Ser Met Leu Lys
335                 340                 345                 350

TCA GAA GAA GAA CGA TTA TCC ATT CAA AAT TTT AGC AAA CTT CTG AAT      1104
Ser Glu Glu Glu Arg Leu Ser Ile Gln Asn Phe Ser Lys Leu Leu Asn
                355                 360                 365

GAC AAC ATT TTT CAT ATG TCT TTA TTG GCG TGC GCT CTT GAG GTT GTA      1152
Asp Asn Ile Phe His Met Ser Leu Leu Ala Cys Ala Leu Glu Val Val
            370                 375                 380

ATG GCC ACA TAT AGC AGA AGT ACA TCT CAG AAT CTT GAT TCT GGA ACA      1200
Met Ala Thr Tyr Ser Arg Ser Thr Ser Gln Asn Leu Asp Ser Gly Thr
        385                 390                 395

GAT TTG TCT TTC CCA TGG ATT CTG AAT GTG CTT AAT TTA AAA GCC TTT      1248
Asp Leu Ser Phe Pro Trp Ile Leu Asn Val Leu Asn Leu Lys Ala Phe
    400                 405                 410

GAT TTT TAC AAA GTG ATC GAA AGT TTT ATC AAA GCA GAA GGC AAC TTG      1296
Asp Phe Tyr Lys Val Ile Glu Ser Phe Ile Lys Ala Glu Gly Asn Leu
415                 420                 425                 430

ACA AGA GAA ATG ATA AAA CAT TTA GAA CGA TGT GAA CAT CGA ATC ATG      1344
Thr Arg Glu Met Ile Lys His Leu Glu Arg Cys Glu His Arg Ile Met
                435                 440                 445

GAA TCC CTT GCA TGG CTC TCA GAT TCA CCT TTA TTT GAT CTT ATT AAA      1392
Glu Ser Leu Ala Trp Leu Ser Asp Ser Pro Leu Phe Asp Leu Ile Lys
            450                 455                 460

CAA TCA AAG GAC CGA GAA GGA CCA ACT GAT CAC CTT GAA TCT GCT TGT      1440
Gln Ser Lys Asp Arg Glu Gly Pro Thr Asp His Leu Glu Ser Ala Cys
        465                 470                 475
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CCT CTT AAT CTT CCT CTC CAG AAT AAT CAC ACT GCA GCA GAT ATG TAT      1488
Pro Leu Asn Leu Pro Leu Gln Asn Asn His Thr Ala Ala Asp Met Tyr
    480                 485                 490

CTT TCT CCT GTA AGA TCT CCA AAG AAA AAA GGT TCA ACT ACG CGT GTA      1536
Leu Ser Pro Val Arg Ser Pro Lys Lys Lys Gly Ser Thr Thr Arg Val
495                 500                 505                 510

AAT TCT ACT GCA AAT GCA GAG ACA CAA GCA ACC TCA GCC TTC CAG ACC      1584
Asn Ser Thr Ala Asn Ala Glu Thr Gln Ala Thr Ser Ala Phe Gln Thr
                515                 520                 525

CAG AAG CCA TTG AAA TCT ACC TCT CTT TCA CTG TTT TAT AAA AAA GTG      1632
Gln Lys Pro Leu Lys Ser Thr Ser Leu Ser Leu Phe Tyr Lys Lys Val
            530                 535                 540

TAT CGG CTA GCC TAT CTC CGG CTA AAT ACA CTT TGT GAA CGC CTT CTG      1680
Tyr Arg Leu Ala Tyr Leu Arg Leu Asn Thr Leu Cys Glu Arg Leu Leu
        545                 550                 555

TCT GAG CAC CCA GAA TTA GAA CAT ATC ATC TGG ACC CTT TTC CAG CAC      1728
Ser Glu His Pro Glu Leu Glu His Ile Ile Trp Thr Leu Phe Gln His
    560                 565                 570

ACC CTG CAG AAT GAG TAT GAA CTC ATG AGA GAC AGG CAT TTG GAC CAA      1776
Thr Leu Gln Asn Glu Tyr Glu Leu Met Arg Asp Arg His Leu Asp Gln
575                 580                 585                 590

ATT ATG ATG TGT TCC ATG TAT GGC ATA TGC AAA GTG AAG AAT ATA GAC      1824
Ile Met Met Cys Ser Met Tyr Gly Ile Cys Lys Val Lys Asn Ile Asp
                595                 600                 605

CTT AAA TTC AAA ATC ATT GTA ACA GCA TAC AAG GAT CTT CCT CAT GCT      1872
Leu Lys Phe Lys Ile Ile Val Thr Ala Tyr Lys Asp Leu Pro His Ala
            610                 615                 620

GTT CAG GAG ACA TTC AAA CGT GTT TTG ATC AAA GAA GAG GAG TAT GAT      1920
Val Gln Glu Thr Phe Lys Arg Val Leu Ile Lys Glu Glu Glu Tyr Asp
        625                 630                 635

TCT ATT ATA GTA TTC TAT AAC TCG GTC TTC ATG CAG AGA CTG AAA ACA      1968
Ser Ile Ile Val Phe Tyr Asn Ser Val Phe Met Gln Arg Leu Lys Thr
    640                 645                 650

AAT ATT TTG CAG TAT GCT TCC ACC AGG CCC CCT ACC TTG TCA CCA ATA      2016
Asn Ile Leu Gln Tyr Ala Ser Thr Arg Pro Pro Thr Leu Ser Pro Ile
655                 660                 665                 670

CCT CAC ATT CCT CGA AGC CCT TAC AAG TTT CCT AGT TCA CCC TTA CGG      2064
Pro His Ile Pro Arg Ser Pro Tyr Lys Phe Pro Ser Ser Pro Leu Arg
                675                 680                 685

ATT CCT GGA GGG AAC ATC TAT ATT TCA CCC CTG AAG AGT CCA TAT AAA      2112
Ile Pro Gly Gly Asn Ile Tyr Ile Ser Pro Leu Lys Ser Pro Tyr Lys
            690                 695                 700
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ATT TCA GAA GGT CTG CCA ACA CCA ACA AAA ATG ACT CCA AGA TCA AGA      2160
Ile Ser Glu Gly Leu Pro Thr Pro Thr Lys Met Thr Pro Arg Ser Arg
        705                 710                 715

ATC TTA GTA TCA ATT GGT GAA TCA TTC GGG ACT TCT GAG AAG TTC CAG      2208
Ile Leu Val Ser Ile Gly Glu Ser Phe Gly Thr Ser Glu Lys Phe Gln
    720                 725                 730

AAA ATA AAT CAG ATG GTA TGT AAC AGC GAC CGT GTG CTC AAA AGA AGT      2256
Lys Ile Asn Gln Met Val Cys Asn Ser Asp Arg Val Leu Lys Arg Ser
735                 740                 745                 750

GCT GAA GGA AGC AAC CCT CCT AAA CCA CTG AAA AAA CTA CGC TTT GAT      2304
Ala Glu Gly Ser Asn Pro Pro Lys Pro Leu Lys Lys Leu Arg Phe Asp
                755                 760                 765

ATT GAA GGA TCA GAT GAA GCA GAT GGA AGT AAA CAT CTC CCA GGA GAG      2352
Ile Glu Gly Ser Asp Glu Ala Asp Gly Ser Lys His Leu Pro Gly Glu
            770                 775                 780

TCC AAA TTT CAG CAG AAA CTG GCA GAA ATG ACT TCT ACT CGA ACA CGA      2400
Ser Lys Phe Gln Gln Lys Leu Ala Glu Met Thr Ser Thr Arg Thr Arg
        785                 790                 795

ATG CAA AAG CAG AAA ATG AAT GAT AGC ATG GAT ACC TCA AAC AAG GAA      2448
Met Gln Lys Gln Lys Met Asn Asp Ser Met Asp Thr Ser Asn Lys Glu
    800                 805                 810

GAG AAA TGAGGATCTC AGGACCTTGG TGGACACTGT GTACACCTCT GGATTCATTG       2504
Glu Lys
815

TCTCTCACAG ATGTGACTGT ATAACTTTCC CAGGTTCTGT TTATGGCCAC ATTTAATATC    2564

TTCAGCTCTT TTTGTGGATA TAAAATGTGC AGATGCAATT GTTTGGGTGA TTCCTAAGCC    2624

ACTTGAAATG TTAGTCATTG TTATTTATAC AAGATTGAAA ATCTTGTGTA AATCCTGCCA    2684

TTTAAAAAGT TGTAGCAGAT TGTTTCCTCT TCCAAAGTAA AATTGCTGTG CTTTATGGAT    2744

AGTAAGAATG GCCCTAGAGT GGGAGTCCTG ATAACCCAGG CCTGTCTGAC TACTTTGCCT    2804

TCTTTTGTAG CATATAGGTG ATGTTTGCTC TTGTTTTTAT TAATTTATAT GTATATTTTT    2864

TTAATTTAAC ATGAACACCC TTAGAAAATG TGTCCTATCT ATCTTCCAAA TGCAATTTGA    2924

TTGACTGCCC ATTCACCAAA ATTATCCTGA ACTCTTCTGC AAAAATGGAT ATTATTAGAA    2984

ATTAGAAAAA AATTACTAAT TTTACACATT AGATTTTATT TTACTATTGG AATCTGATAT    3044

ACTGTGTGCT TGTTTTATAA AATTTTGCTT TTAATTAAAT AAAAGCTGGA AGCAAAGTAT    3104

AACCATATGA TACTATCATA CTACTGAAAC AGATTTCATA CCTCAGAATG TAAAAGAACT    3164

TACTGATTAT TTTCTTCATC CAACTTATGT TTTTAAATGA GGATTATTGA TAGT          3218
```

(2) INFORMATION FOR SEQ ID NO: 4:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 816 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

```
Met Ser Phe Thr Phe Thr Glu Leu Gln Lys Asn Ile Glu Ile Ser Val
 1               5                  10                  15

His Lys Phe Phe Asn Leu Leu Lys Glu Ile Asp Thr Ser Thr Lys Val
            20                  25                  30

Asp Asn Ala Met Ser Arg Leu Leu Lys Lys Tyr Asp Val Leu Phe Ala
        35                  40                  45

Leu Phe Ser Lys Leu Glu Arg Thr Cys Glu Leu Ile Tyr Leu Thr Gln
    50                  55                  60

Pro Ser Ser Ser Ile Ser Thr Glu Ile Asn Ser Ala Leu Val Leu Lys
65                  70                  75                  80

Val Ser Trp Ile Thr Phe Leu Leu Ala Lys Gly Glu Val Leu Gln Met
                85                  90                  95

Glu Asp Asp Leu Val Ile Ser Phe Gln Leu Met Leu Cys Val Leu Asp
            100                 105                 110

Tyr Phe Ile Lys Leu Ser Pro Pro Met Leu Leu Lys Glu Pro Tyr Lys
        115                 120                 125

Thr Ala Val Ile Pro Ile Asn Gly Ser Pro Arg Thr Pro Arg Arg Gly
    130                 135                 140

Gln Asn Arg Ser Ala Arg Ile Ala Lys Gln Leu Glu Asn Asp Thr Arg
145                 150                 155                 160

Ile Ile Glu Val Leu Cys Lys Glu His Glu Cys Asn Ile Asp Glu Val
                165                 170                 175

Lys Asn Val Tyr Phe Lys Asn Phe Ile Pro Phe Met Asn Ser Leu Gly
            180                 185                 190

Leu Val Thr Ser Asn Gly Leu Pro Glu Val Glu Asn Leu Ser Lys Arg
        195                 200                 205

Tyr Glu Glu Ile Tyr Leu Lys Asn Lys Asp Leu Asp Ala Arg Leu Phe
    210                 215                 220

Leu Asp His Asp Lys Thr Leu Gln Thr Asp Ser Ile Asp Ser Phe Glu
225                 230                 235                 240

Thr Gln Arg Thr Pro Arg Lys Ser Asn Leu Asp Glu Glu Val Asn Val
                245                 250                 255
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Ile Pro Pro His Thr Pro Val Arg Thr Val Met Asn Thr Ile Gln Gln
            260                 265                 270

Leu Met Met Ile Leu Asn Ser Ala Ser Asp Gln Pro Ser Glu Asn Leu
        275                 280                 285

Ile Ser Tyr Phe Asn Asn Cys Thr Val Asn Pro Lys Glu Ser Ile Leu
    290                 295                 300

Lys Arg Val Lys Asp Ile Gly Tyr Ile Phe Lys Glu Lys Phe Ala Lys
305                 310                 315                 320

Ala Val Gly Gln Gly Cys Val Glu Ile Gly Ser Gln Arg Tyr Lys Leu
                325                 330                 335

Gly Val Arg Leu Tyr Tyr Arg Val Met Glu Ser Met Leu Lys Ser Glu
            340                 345                 350

Glu Glu Arg Leu Ser Ile Gln Asn Phe Ser Lys Leu Leu Asn Asp Asn
        355                 360                 365

Ile Phe His Met Ser Leu Leu Ala Cys Ala Leu Glu Val Val Met Ala
    370                 375                 380

Thr Tyr Ser Arg Ser Thr Ser Gln Asn Leu Asp Ser Gly Thr Asp Leu
385                 390                 395                 400

Ser Phe Pro Trp Ile Leu Asn Val Leu Asn Leu Lys Ala Phe Asp Phe
                405                 410                 415

Tyr Lys Val Ile Glu Ser Phe Ile Lys Ala Glu Gly Asn Leu Thr Arg
            420                 425                 430

Glu Met Ile Lys His Leu Glu Arg Cys Glu His Arg Ile Met Glu Ser
        435                 440                 445

Leu Ala Trp Leu Ser Asp Ser Pro Leu Phe Asp Leu Ile Lys Gln Ser
    450                 455                 460

Lys Asp Arg Glu Gly Pro Thr Asp His Leu Glu Ser Ala Cys Pro Leu
465                 470                 475                 480

Asn Leu Pro Leu Gln Asn Asn His Thr Ala Ala Asp Met Tyr Leu Ser
                485                 490                 495

Pro Val Arg Ser Pro Lys Lys Lys Gly Ser Thr Thr Arg Val Asn Ser
            500                 505                 510

Thr Ala Asn Ala Glu Thr Gln Ala Thr Ser Ala Phe Gln Thr Gln Lys
        515                 520                 525

Pro Leu Lys Ser Thr Ser Leu Ser Leu Phe Tyr Lys Lys Val Tyr Arg
    530                 535                 540

Leu Ala Tyr Leu Arg Leu Asn Thr Leu Cys Glu Arg Leu Leu Ser Glu
545                 550                 555                 560
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His Pro Glu Leu Glu His Ile Ile Trp Thr Leu Phe Gln His Thr Leu
                565                 570                 575

Gln Asn Glu Tyr Glu Leu Met Arg Asp Arg His Leu Asp Gln Ile Met
            580                 585                 590

Met Cys Ser Met Tyr Gly Ile Cys Lys Val Lys Asn Ile Asp Leu Lys
        595                 600                 605

Phe Lys Ile Ile Val Thr Ala Tyr Lys Asp Leu Pro His Ala Val Gln
    610                 615                 620

Glu Thr Phe Lys Arg Val Leu Ile Lys Glu Glu Glu Tyr Asp Ser Ile
625                 630                 635                 640

Ile Val Phe Tyr Asn Ser Val Phe Met Gln Arg Leu Lys Thr Asn Ile
                645                 650                 655

Leu Gln Tyr Ala Ser Thr Arg Pro Pro Thr Leu Ser Pro Ile Pro His
            660                 665                 670

Ile Pro Arg Ser Pro Tyr Lys Phe Pro Ser Ser Pro Leu Arg Ile Pro
        675                 680                 685

Gly Gly Asn Ile Tyr Ile Ser Pro Leu Lys Ser Pro Tyr Lys Ile Ser
    690                 695                 700

Glu Gly Leu Pro Thr Pro Thr Lys Met Thr Pro Arg Ser Arg Ile Leu
705                 710                 715                 720

Val Ser Ile Gly Glu Ser Phe Gly Thr Ser Glu Lys Phe Gln Lys Ile
                725                 730                 735

Asn Gln Met Val Cys Asn Ser Asp Arg Val Leu Lys Arg Ser Ala Glu
            740                 745                 750

Gly Ser Asn Pro Pro Lys Pro Leu Lys Lys Leu Arg Phe Asp Ile Glu
        755                 760                 765

Gly Ser Asp Glu Ala Asp Gly Ser Lys His Leu Pro Gly Glu Ser Lys
    770                 775                 780

Phe Gln Gln Lys Leu Ala Glu Met Thr Ser Thr Arg Thr Arg Met Gln
785                 790                 795                 800

Lys Gln Lys Met Asn Asp Ser Met Asp Thr Ser Asn Lys Glu Glu Lys
                805                 810                 815
```

(2) INFORMATION FOR SEQ ID NO: 5:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

AAGATCTAGG CTGCCTGGAT CCT 23

(2) INFORMATION FOR SEQ ID NO: 6:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

AGGATCCAGG CAGCCTAGAT CTT 23

(2) INFORMATION FOR SEQ ID NO: 7:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 285 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

CTCGAGCAAT GGGCGTGATA GCGGTTTGAC TCACGGGGAT TTCCAAGTCT CCACCCCATT 60

GACGTCAATG GGAGTTTGTT TTGGCACCAA AATCAACGGG ACTTTCCAAA ATGTCGTAAC 120

AACTCCGCCC CATTGACGCA AATGGGCGGT AGGCGTGTAC GGTGGGAGGT CTATATAAGC 180

AGAGCTCGTT TAGTGAACCG TCAGATCGCC TGGAGACGCC ATCCACGCTG TTTTGACCTC 240

CATAGAAGAC ACCGGGACCG ATCCAGCCTC CGCGGCCGCG AATTC 285

(2) INFORMATION FOR SEQ ID NO: 8:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 28 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

CCGCTCGAGC AATGGGCGTG GATAGCGG 28

(2) INFORMATION FOR SEQ ID NO: 9:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

CCGCTCGAGC ACCAAAATCA ACGGGA 26

(2) INFORMATION FOR SEQ ID NO: 10:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 27 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

CCGCTCGAGC AACTCCGCCC CATTGAC 27

(2) INFORMATION FOR SEQ ID NO: 11:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

TAGACATATG AATTCGCGGC C 21

(2) INFORMATION FOR SEQ ID NO: 12:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

CTAGAATTCG CTGTCTGCG 19

(2) INFORMATION FOR SEQ ID NO: 13:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

GCTCTAGATG CAGTTGGACC TGGGAG 26

(2) INFORMATION FOR SEQ ID NO: 14:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 32 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

CCCAAGCTTG CCGCCATGTC GTTCACTTTT AC 32

(2) INFORMATION FOR SEQ ID NO: 15:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:

GTCCAAGAGA ATTCATAAAA GG 22

(2) INFORMATION FOR SEQ ID NO: 16:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 39 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:

CCCAAGCTTG CCGCCATGGA GCAGGACAGC GGCCCGGAC 39

(2) INFORMATION FOR SEQ ID NO: 17:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 39 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:

CCCAAGCTTG CCGCCATGGA TTTTACTGCA TTATGTCAG 39

(2) INFORMATION FOR SEQ ID NO: 18:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 39 base pairs
(B) TYPE: nucleic acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18:

CCCAAGCTTG CCGCCATGGA GAAAGTTTCA TCTTGTGAT 39

(2) INFORMATION FOR SEQ ID NO: 19:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 39 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 19:

CCCAAGCTTG CCGCCATGCT GTGGGGAATC TGTATCTTT 39

(2) INFORMATION FOR SEQ ID NO: 20:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 36 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 20:

CCCAAGCTTG CCGCCATGTC AAGACTGTTG AAGAAG 36

(2) INFORMATION FOR SEQ ID NO: 21:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 30 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 21:

GCGCCTGAGG ACCTAGATGA GATGTCGTTC 30

(2) INFORMATION FOR SEQ ID NO: 22:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 31 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 22:

GCGGTTAACC CTAGATGAGA TGTCGTTCAC T 31

(2) INFORMATION FOR SEQ ID NO: 23:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 36 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 23:

CCCAAGCTTG CCGTCATGCC GCCCAAAACC CCCCGA 36

(2) INFORMATION FOR SEQ ID NO: 24:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 24:

CTCACCTAGG TCAACTGCTG CAAT 24

(2) INFORMATION FOR SEQ ID NO: 25:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 25:

GTTGACCTAG GTGATATGTC GTTC 24

(2) INFORMATION FOR SEQ ID NO: 26:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 31 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 26:

GCGCCTAGGA TCTACTGAAA TAAATTCTGC A 31

(2) INFORMATION FOR SEQ ID NO: 27:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 31 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 27:

CCCGATATCA ACTGCTGGGT TGTGTCAAAT A 31

(2) INFORMATION FOR SEQ ID NO: 28:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 32 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 28:

CCCGAATTCG TTTTATATGG TTCTTTGAGC AA 32

(2) INFORMATION FOR SEQ ID NO: 29:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ix) FEATURE:
(A) NAME/KEY: modified_base
(B) LOCATION:4..5
(D) OTHER INFORMATION:/note= "R=A or G"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 29:

GCCRCCAUGG 10

(2) INFORMATION FOR SEQ ID NO: 30:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 30:

CTCGAGCCAA GACCTGGCCC AG 22

(2) INFORMATION FOR SEQ ID NO: 31:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 base pairs
(B) TYPE: nucleic acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 31:

ATCTAGATGG TCGACTTGTC TGT 23

CLAIMS:

1. A tetracycline responsive expression vector comprising a first sequence region encoding a fusion protein comprising a transcriptional transactivation domain operatively attached to a tetracycline repressor protein, said first sequence region operatively positioned downstream of a promoter; said vector further comprising a second sequence region comprising a cloning site operatively positioned downstream of a basal promoter comprising a tetracycline operator nucleic acid sequence.

2. The expression vector of claim 1, wherein said first sequence region operatively positioned downstream of a minimal promoter.

3. A tetracycline responsive expression vector comprising a minimal promoter operatively positioned upstream of a first sequence region comprising a fusion protein gene encoding a fusion protein that comprises a transcriptional transactivation domain operatively attached to a tetracycline repressor protein.

4. A tetracycline responsive expression system comprising:

a) a first nucleic acid vector comprising a minimal promoter operatively positioned upstream of a first sequence region encoding a fusion protein comprising a transcriptional transactivation domain operatively attached to a tetracycline repressor protein; and

b) a second nucleic acid vector comprising a basal promoter comprising a tetracycline operator nucleic acid sequence, operatively positioned upstream of a second sequence region comprising a cloning site.

5. A tetracycline responsive expression system comprising a first sequence region comprising a fusion protein gene encoding a fusion protein that comprises a transcriptional transactivation domain operatively attached to a tetracycline repressor protein, said first sequence region operatively positioned downstream of a minimal promoter; and a second sequence region comprising a cloning site operatively positioned downstream of a basal promoter comprising a tetracycline operator nucleic acid sequence.

6. The expression vector or system of claim 4, wherein said first sequence region and said second sequence region are comprised within a single nucleic acid vector.

7. The expression vector or system of claim 4, wherein said first sequence region is comprised within a first nucleic acid vector, and said second sequence region is comprised within a second nucleic acid vector.

8. The expression vector or system of any one of claims 2-7, wherein said minimal promoter is a minimal CMV promoter.

9. The expression vector or system of claim 8, wherein said minimal CMV promoter comprises the sequence of SEQ ID NO:7.

10. The expression vector or system of claim 8, wherein said minimal promoter has between about 1% and about 50% of the promoter activity of the CMV promoter.

11. The expression vector or system of claim 10, wherein said minimal promoter has about 18% of the promoter activity of the CMV promoter.

12. The expression vector or system of claim 10, wherein said minimal promoter has about 3% of the promoter activity of the CMV promoter.

13. The expression vector or system of any preceeding claim, further comprising a marker gene encoding a selectable marker protein.

14. The expression vector or system of claim 13; wherein said marker gene confers resistance to G418.

15. The expression vector or system of any preceeding claim, wherein the transcriptional activation domain of said fusion protein is a viral transcriptional transactivation domain.

16. The expression vector or system of claim 15, wherein said transcriptional transactivation domain is the VP16 protein transcriptional transactivation domain.

17. The expression vector or system of any one of claims 1-14, wherein the transcriptional activation domain of said fusion protein is a eukaryotic transcriptional transactivation domain.

18. The expression vector or system of claim 17, wherein said transcriptional transactivation domain is a yeast transcriptional transactivation domain.

19. The expression vector or system of claim 18, wherein said transcriptional transactivation domain is the GAL4 protein transcriptional transactivation domain.

20. The expression vector or system of any one of claims 1, 4 or 5, wherein at least a first exogenous DNA segment is inserted into said cloning site.

21. The expression vector or system of claim 20, wherein said first exogenous DNA segment encodes a pharmaceutically active protein.

22. The expression vector or system of claim 21, wherein said first exogenous DNA segment comprises a gene encoding a tumor suppressor protein.

23. The expression vector or system of claim 22, wherein said first exogenous DNA segment comprises a gene encoding a retinoblastoma protein.

24. The expression vector or system of claim 23, wherein said first exogenous DNA segment comprises a gene encoding a truncated or mutant retinoblastoma protein.

25. The expression vector or system of claim 22, wherein said first exogenous DNA segment comprises a gene encoding a p53 protein.

26. The expression vector or system of claim 25, wherein said first exogenous DNA segment comprises a gene encoding a truncated or mutant p53 protein.

27. The expression vector or system of claim 21, wherein said first exogenous DNA segment comprises a gene encoding a cytokine.

28. The expression vector or system of claim 27, wherein said gene encodes TNFα, an interferon or an interleukin.

29. The expression vector or system of any preceeding claim, comprised within a single adenoviral vector.

30. The expression vector or system of claim 29, wherein said adenovirus vector is comprised within a recombinant adenovirus.

31. The expression vector or system of any one of claims 1-28, comprised within a single retroviral vector.

32. The expression vector or system of claim 31, wherein said retrovirus vector is comprised within a recombinant retrovirus.

33. The expression vector or system of any preceeding claim, dispersed in a pharmaceutically acceptable excipient.

34. The expression vector or system of any preceeding claim, comprised within a host cell.

35. The expression vector or system of claim 34, wherein said host cell is a eukaryotic host cell.

36. The expression vector or system of claim 35, wherein said host cell is a human cell.

37. The expression vector or system of claim 35, wherein said host cell is a tumor cell.

38. An improved tetracycline responsive expression system, wherein the improvement comprises the use of a minimal promoter to express a fusion protein comprising a transcriptional transactivation domain operatively attached to a tetracycline repressor protein.

39. The improved tetracycline responsive expression system of claim 38, wherein said minimal promoter has between about 1% and about 50% of the promoter activity of the CMV promoter.

40. The tetracycline responsive expression vector or system of any prceeding claim for use in expressing a nucleic acid segment encoding a selected protein.

41. Use of a tetracycline responsive expression vector or system in accordance with any one of claims 1-39 in the expression of a nucleic acid segment encoding a selected protein.

42. The tetracycline responsive expression vector or system of any one of claims 1-39 for use in inhibiting cellular proliferation.

43. Use of a tetracycline responsive expression vector or system in accordance with any one of claims 1-39 in inhibiting cellular proliferation.

44. The tetracycline responsive expression vector or system of any one of claims 1-39 for use in the preparation of a medicament for inhibiting cellular proliferation.

45. Use of a tetracycline responsive expression vector or system in accordance with any one of claims 1-39 in the preparation of a medicament for inhibiting cellular proliferation.

46. The tetracycline responsive expression vector or system of any one of claims 1-39 for use in the preparation of a medicament for treating cancer.

47. Use of a tetracycline responsive expression vector or system in accordance with any one of claims 1-39 in the preparation of a medicament for treating cancer.

48. A recombinant host cell comprising a tetracycline responsive expression vector or system in accordance with any one of claims 1-39.

49. The host cell of claim 48, wherein said host cell is a eukaryotic cell.

50. The host cell of claim 49, wherein said host cell is a human cell.

51. The host cell of claim 49, wherein said human cell is a tumor cell.

52. The host cell of claim 48, wherein said tetracycline responsive expression vector or system is introduced into said cell by means of a recombinant adenovirus or retrovirus vector.

53. A pharmaceutical composition comprising a tetracycline responsive expression vector or system in accordance with any one of claims 1-39.

54. The pharmaceutical composition of claim 53, wherein said tetracycline responsive expression vector or system further comprises a first exogenous DNA segment encoding a tumor suppressor protein or a cytokine.

55. The pharmaceutical composition of claim 54, wherein said tetracycline responsive expression vector or system is comprised within a viral vector.

56. The pharmaceutical composition of claim 55, wherein said viral vector is comprised within a virus.

57. A method of producing a selected protein in a cell, comprising providing to said cell a tetracycline responsive expression system comprising a first sequence region comprising an isolated gene encoding a fusion protein comprising a transcriptional transactivation domain operatively attached to a tetracycline repressor protein, said first sequence region operatively positioned downstream of a minimal promoter; and a second sequence region comprising a nucleic acid segment encoding said selected protein operatively positioned downstream of a promoter comprising a tetracycline operator nucleic acid sequence and collecting the protein produced.

58. The method of claim 57, wherein said cell is a eukaryotic cell.

59. The method of claim 57, wherein said selected protein is a tumor suppressor protein or a cytokine.

60. The method of claim 57, wherein said tetracycline responsive expression system is provided to said cell by means of a recombinant adenovirus vector or a recombinant retrovirus vector.

61. A method of inhibiting cellular proliferation, comprising providing to a cell a tetracycline responsive expression system that expresses an effective amount of a proliferation inhibiting protein in said cell; said expression system comprising:

(a) a first sequence region comprising an isolated gene encoding a fusion protein comprising a transcriptional transactivation domain operatively attached to a tetracycline repressor protein, said first sequence region operatively positioned downstream of a minimal promoter; and

(b) a second sequence region comprising a cloning site for insertion of at least a first exogenous DNA segment, said first exogenous DNA segment encoding said proliferation inhibiting protein, said cloning site operatively positioned downstream of a promoter comprising a tetracycline operator nucleic acid sequence.

62. The method of claim 61, wherein said proliferation inhibiting protein is a tumor suppressor protein or a cytokine.

63. The method of claim 61, wherein said tetracycline responsive expression system is comprised within an adenovirus vector or a retrovirus vector.

64. The method of claim 61, wherein said cell is a tumor cell.

65. The method of claim 61, wherein said cell is located within an animal and said cell is provided with said expression system by administering an effective amount of said expression system to said animal in a pharmaceutically acceptable vehicle.

66. The method of claim 65, wherein said animal is a human subject.

67. The method of claim 61, wherein said expression system further comprises at least a second exogenous DNA segment that encodes at least a second protein that inhibits cellular proliferation.

68. A DNA segment comprising an isolated gene encoding a modified p53 tumor suppressor protein comprising an N-terminal modification.

69. The DNA segment of claim 68, wherein said gene encodes a modified p53 tumor suppressor protein comprising an N-terminal region that comprises a first sequence region from which at least one amino acid has been deleted.

70. The DNA segment of claim 69, wherein at least two amino acids have been deleted from said first sequence region.

71. The DNA segment of claim 70, wherein at least about 25 amino acids have been deleted from said first sequence region.

72. The DNA segment of claim 71, wherein at least about 100 amino acids have been deleted from said first sequence region.

73. The DNA segment of claim 69, wherein said first sequence region is located between about amino acid 1 and about amino acid 50, between about amino acid 51 and about amino acid 100 or between about amino acid 1 and about amino acid 100.

74. The DNA segment of claim 69, wherein said N-terminal region of said modified p53 tumor suppressor protein further comprises a second sequence region from which at least one amino acid has been deleted.

75. The DNA segment of claim 68, wherein said gene encodes a modified p53 tumor suppressor protein comprising at least a first N-terminal mutation, and wherein said modified p53 tumor suppressor protein has an increased biological activity in comparison to the biological activity of the corresponding wild-type p53 tumor suppressor protein.

76. The DNA segment of claim 75, wherein said modified p53 tumor suppressor protein comprises at least a second N-terminal mutation.

77. The DNA segment of claim 68, wherein said gene encodes a modified p53 tumor suppressor protein comprising an N-terminal region from which at least one amino acid has been deleted, and which contains at least one amino acid mutation.

78. The DNA segment of claim 68, operationally positioned under the control of a promoter.

79. The DNA segment of claim 78, further defined as a recombinant vector.

80. The DNA segment of claim 68, comprised within a host cell.

81. The DNA segment of claim 68, dispersed in a pharmaceutically acceptable excipient.

82. A modified p53 tumor suppressor protein comprising an N-terminal modification, wherein said modified p53 tumor suppressor protein has a biological activity at least about equivalent to the biological activity of the corresponding wild-type p53 tumor suppressor protein.

83. A recombinant host cell comprising a DNA segment comprising an isolated gene encoding a modified p53 tumor suppressor protein comprising an N-terminal modification.

84. A method of inhibiting cellular proliferation, comprising contacting a cell with an effective inhibitory amount of at least a first modified p53 tumor suppressor protein comprising an N-terminal modification.

85. The method of claim 84, wherein said cell is contacted with said first modified p53 tumor suppressor protein by providing to said cell a DNA segment that expresses said first modified p53 tumor suppressor protein in said cell.

86. The method of claim 84, wherein said cell is located within an animal and said first modified p53 tumor suppressor protein, or a gene encoding said modified p53 tumor suppressor protein, is administered to said animal in a pharmaceutically acceptable vehicle.

87. A method of treating cancer, comprising administering to an animal with cancer a pharmaceutically acceptable composition comprising a biologically effective inhibitory amount of at least a first modified p53 tumor suppressor protein comprising an N-terminal modification.

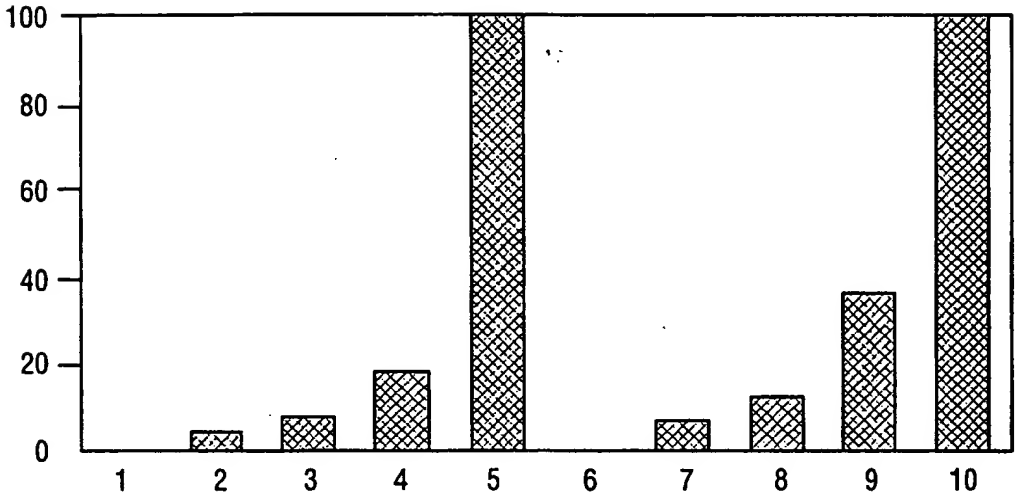


FIG. 1

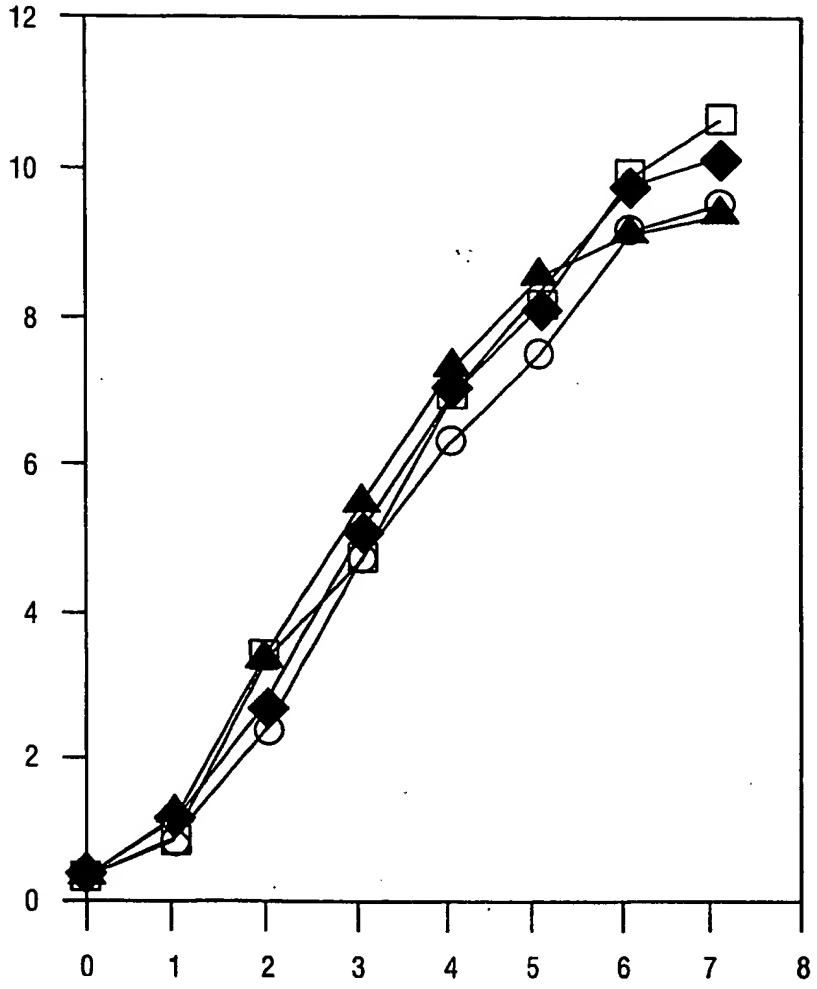


FIG. 2

FIG. 3A

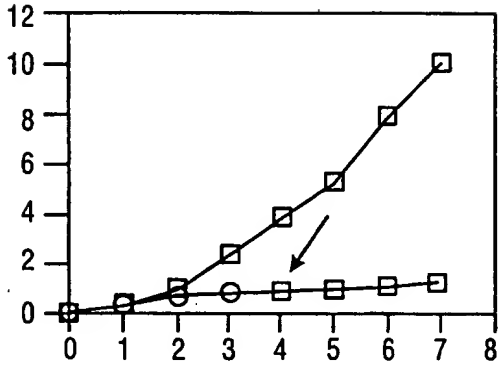


FIG. 3B

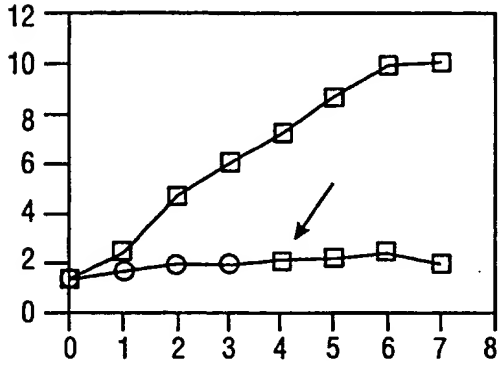


FIG. 3C

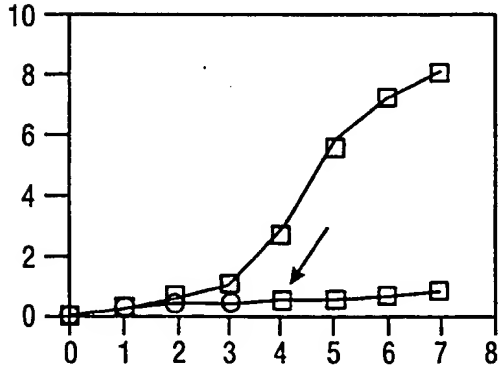


FIG. 4A

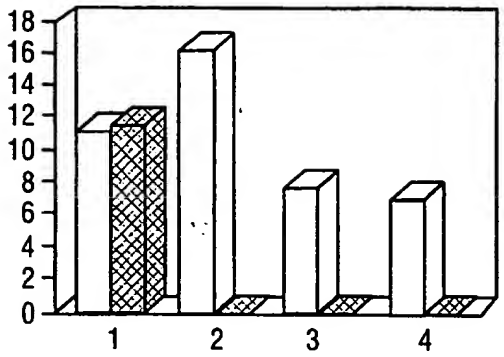


FIG. 4B

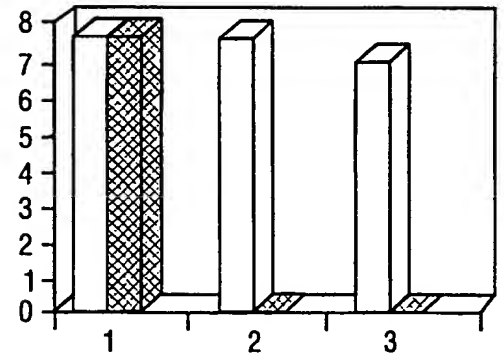
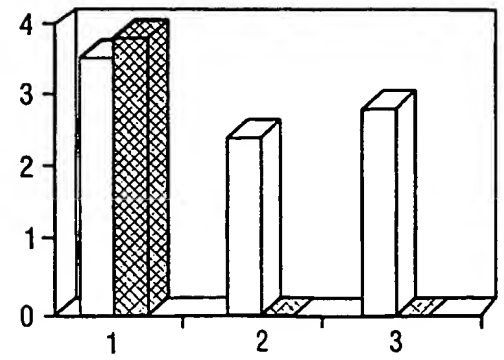


FIG. 4C



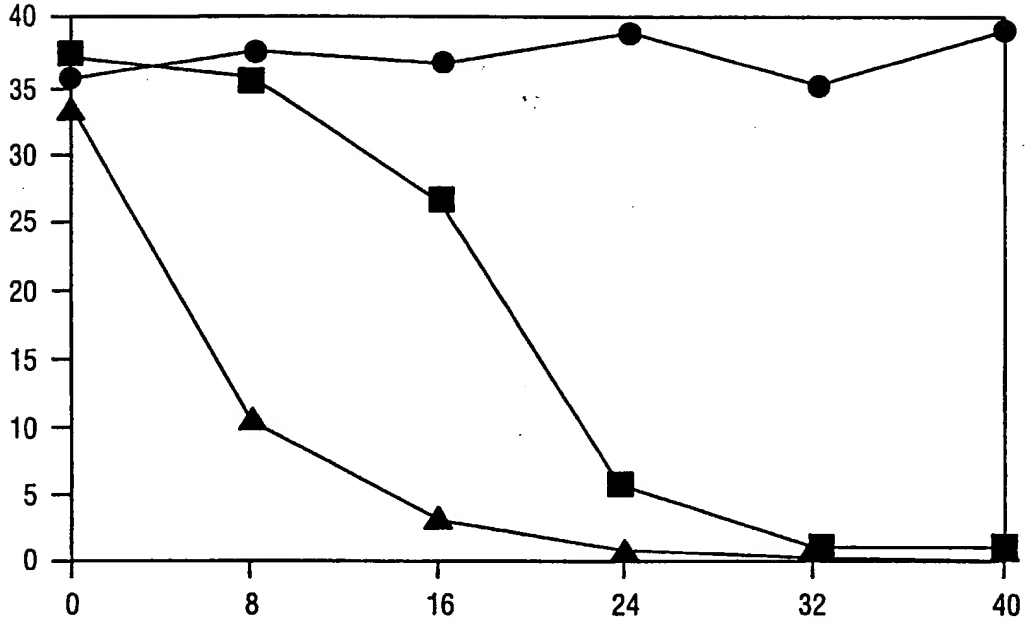


FIG. 5

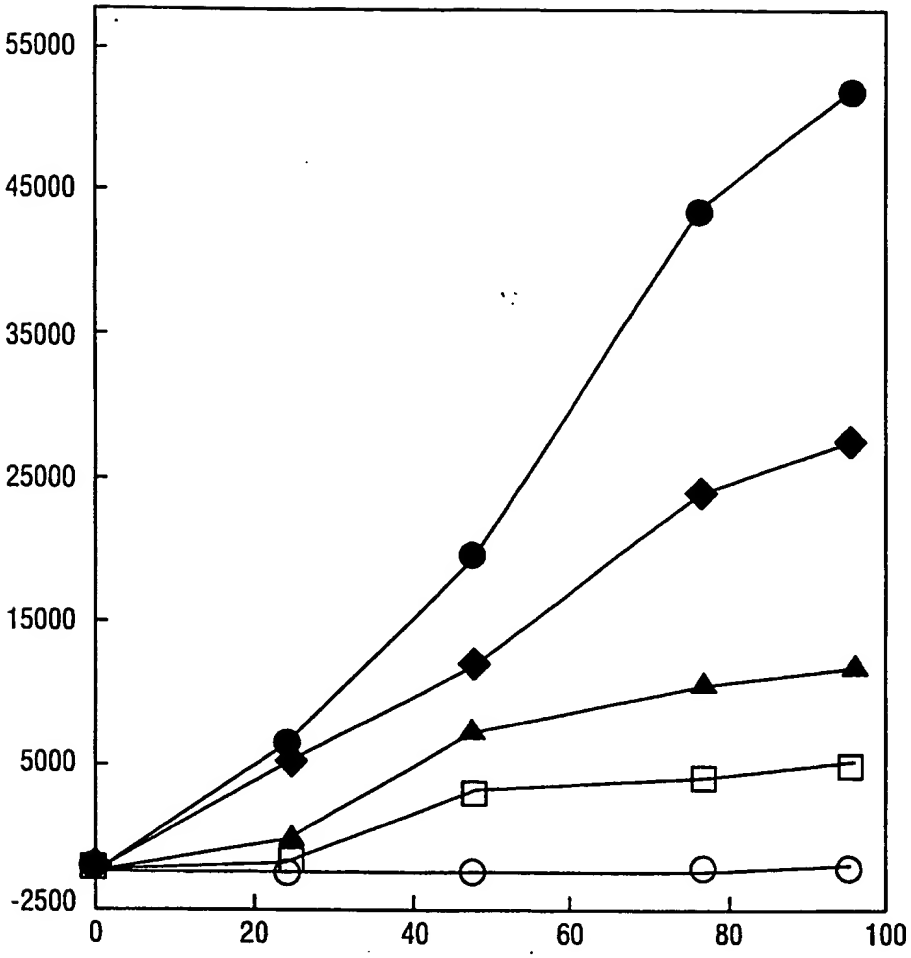


FIG. 6

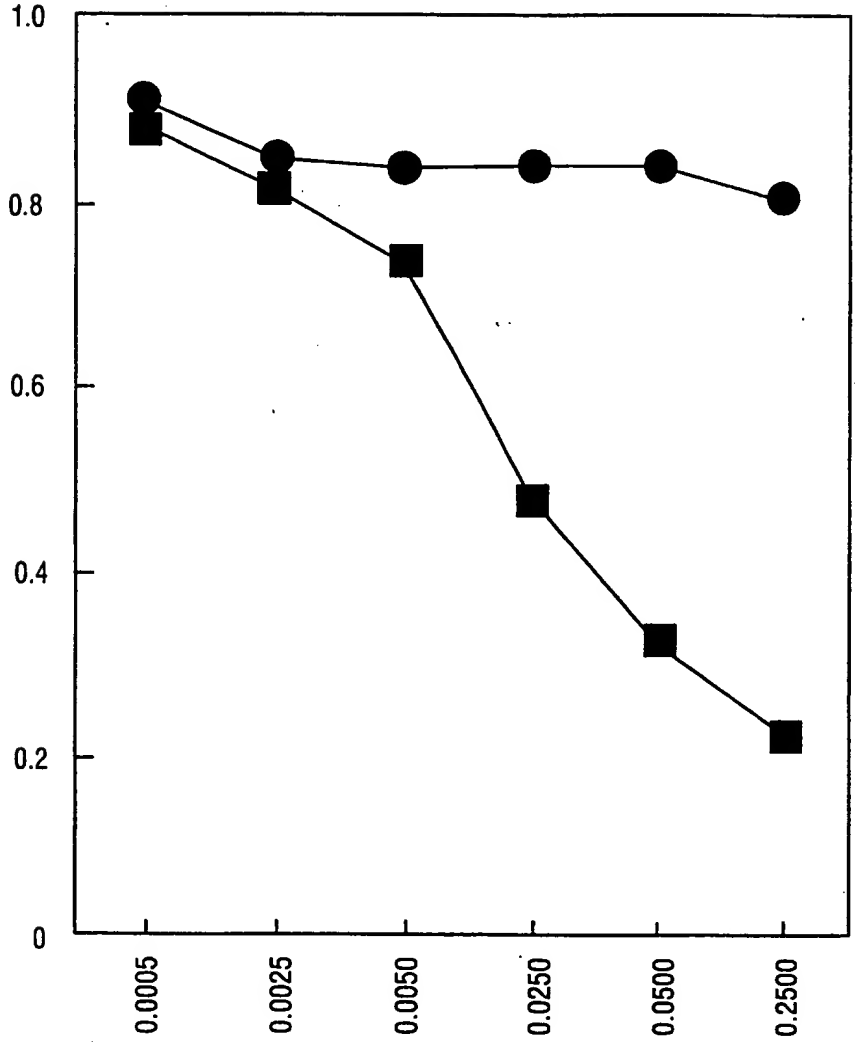


FIG. 7

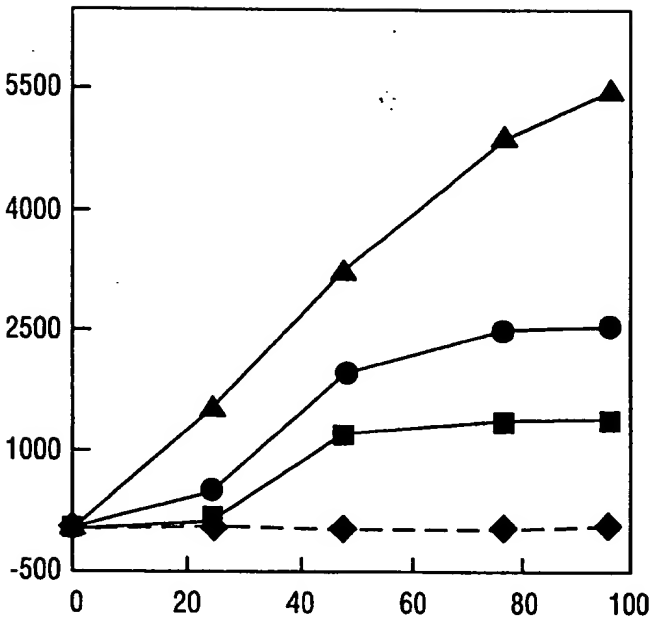


FIG. 8

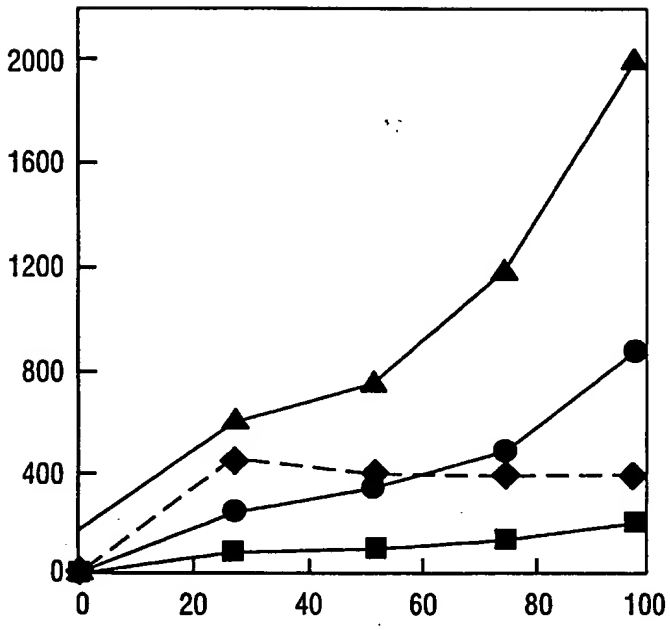


FIG. 9